

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:45:11 ; Search time 55 seconds
(without alignments)
2352.850 Million cell updates/sec

Title: US-10-087-993a-36
Perfect score: 458
Sequence: 1 MSRSLSARSFLERLARGG.....NLRIGRPKGRPPAEWTRV 458

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 1586107 seqs, 282547505 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	418	91.3	458	2 AAW49908	AAW49908 Human bra
2	217	47.4	353	7 ADC99051	ADC99051 Human kpp
3	155	33.8	155	2 AAW37255	AAW37255 Partial h
4	32	7.0	453	2 AAW37254	AAW37254 Novel non
5	29	6.3	453	2 AAW49906	AAW49906 Rat prote
6	20	4.4	20	2 AAW71596	AAW71596 Protein t
7	20	4.4	20	3 AAY81930	AAY81930 Peptide f
8	20	4.4	20	3 AAB08487	AAB08487 Peptide d
9	12	2.6	64	5 ABP07829	ABP07829 Human CRF
10	11	2.4	60	5 ABP04248	ABP04248 Human CRF
11	11	2.4	242	4 AAB59384	AAB59384 Human pro
12	11	2.4	291	4 AAG78282	AAG78282 Human PTP
13	11	2.4	303	5 ABR52340	ABR52340 Protein r
14	11	2.4	692	2 AAY28653	AAY28653 Human Cyt
15	11	2.4	799	4 AAG78623	AAG78623 Human tyr
16	11	2.4	802	2 AAY28654	AAY28654 Murine Cy
17	11	2.4	807	2 AAW89247	AAW89247 Human PTP
18	11	2.4	808	2 AAY28652	AAY28652 Human Cyt
19	11	2.4	913	2 AAW12522	AAW12522 Protein t
20	11	2.4	913	2 AAY28156	AAY28156 Human PTP
21	11	2.4	913	5 AAG79333	AAG79333 PTPH1. 8/
22	11	2.4	913	7 ADD22982	ADD22982 Human pro
23	10	2.2	20	2 AAW71599	AAW71599 Protein t
24	10	2.2	20	3 AAY81933	AAY81933 Peptide f
25	10	2.2	20	3 AAB08490	AAB08490 Peptide d

26 10 2.2 31 3 AAY67255 Aay67255 Pro 1 reg
27 10 2.2 31 3 AAY67254 Aay67254 Pro 1 reg
28 10 2.2 127 2 AAW35301 Aaw35301 Human pol
29 10 2.2 237 7 ADC64297 Adc64297 Human sld
30 10 2.2 253 4 AAB59383 Aab59383 Human pro
31 10 2.2 296 7 ABM78984 Abm78984 Human leu
32 10 2.2 298 2 AAW35300 Aaw35300 Human lsl
33 10 2.2 306 4 AAG78268 Aag78268 Human dca
34 10 2.2 312 4 AAG78281 Aag78281 Human ptp
35 10 2.2 370 2 AAW18093 Aaw18093 Type 1 di
36 10 2.2 376 2 AAW53302 Aaw53302 Human lsl
37 10 2.2 607 3 AAY81783 Aay81783 Human pro
38 10 2.2 641 2 AAW35298 Aaw35298 LAR tyros
39 10 2.2 641 2 AAY56098 Aay56098 Macaque i
40 10 2.2 647 4 AAM23746 Aam23746 Human bst
41 10 2.2 647 4 AAU14379 Aau14379 Human nov
42 10 2.2 723 2 AAW25172 Aaw25172 Mouse ins
43 10 2.2 773 5 ABB57374 Abb57374 Mouse lsc
44 10 2.2 775 3 AAY67250 Aay67250 Mouse pro
45 10 2.2 780 3 AAY67252 Aay67252 Human pro

ALIGNMENTS

RESULT 1
AAW49908
ID AAW49908 standard; protein; 458 AA.
XX
AC AAW49908;
XX
DT 20-JUL-1998 (first entry)
XX
DE Human brain derived phosphatase 1 (BDP-1).
XX
KW Brain derived phosphatase 1; BDP-1; human; receptor;
KW protein tyrosine phosphatase; signal transduction; therapy; diagnosis.
XX
OS Homo sapiens.
XX
PN WO9748723-A2.
XX
PD 24-DEC-1997.
XX
PF 17-JUN-1997; 97WO-IB000946.
XX
PR 17-JUN-1996; 96US-0019629P.
PR 09-AUG-1996; 96US-0023485P.
PR 13-NOV-1996; 96US-0030860P.
PR 15-NOV-1996; 96US-0030964P.
PR 19-DEC-1996; 96US-0034286P.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Ullrich A, Kharitonkov AI, Aoki N, Wang HY, Chen Z, Nayler O;
PI Kim YW;
XX
XX WPI; 1998-120302/11.
DR N-PSDB; AAV17099.
XX
PT New phosphatase and kinase enzyme(s) - useful in the diagnosis and
PT treatment of signal transduction disorders.
XX
PS Claim 11; Fig 3a-d; 138pp; English.
XX
CC This polypeptide comprises a novel human protein tyrosine phosphatase
CC (PTP), designated brain derived phosphatase 1 (BDP-1), that is expressed
CC in most tissues and cell lines at basal level, but expressed high in
CC epithelium origin cell lines and cancer cell lines. The amino acid
CC sequence was deduced from a cDNA clone (see AAV17099) isolated from a
CC haematopoietic MEG01 cDNA library. The invention relates to novel
CC proteins (see AAW49906-14) involved in cellular signal transduction and
CC to the nucleic acids (see AAV17097-99) coding for them, and provides

CC vectors, host cells, purified recombinant proteins, methods for
 CC identifying compounds that activate or inhibit the novel proteins, as
 CC well as methods for the diagnosis and treatment of diseases associated
 CC with the novel proteins
 XX
 SQ Sequence 458 AA;

Query Match 91.3%; Score 418; DB 2; Length 458;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 418; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 KADGVCSVAGSRPENVRKRYKDVLPYDQTRVLSLQEGHSDYINGNFIKGVDSLA 100
 DB 41 KADGVCSVAGSRPENVRKRYKDVLPYDQTRVLSLQEGHSDYINGNFIKGVDSLA 100

QY 101 YIATGGPLPHTLLDFWRLWFEFGVKVILMACREIENGKRCERYWAOEPLQTLFCIT 160
 DB 101 YIATGGPLPHTLLDFWRLWFEFGVKVILMACREIENGKRCERYWAOEPLQTLFCIT 160

QY 161 LIKEKWLNEIDIMLRTLVKVTFOKESRVYQYMSWPDGVPSSPDHMLAVVEARLQGS 220
 DB 161 LIKEKWLNEIDIMLRTLVKVTFOKESRVYQYMSWPDGVPSSPDHMLAVVEARLQGS 220

QY 221 GPEPLVHCSCAGCGTGVLTVDVYVROLITQMIIPDFSLFDVVLKMKRQPAVQTEEQ 280
 DB 221 GPEPLVHCSCAGCGTGVLTVDVYVROLITQMIIPDFSLFDVVLKMKRQPAVQTEEQ 280

QY 281 YRFYHTVAQFCTLQNASPHYQIKENCAPLYDDALFRTQALLAIIRPPGGVLSI 340
 DB 281 YRFYHTVAQFCTLQNASPHYQIKENCAPLYDDALFRTQALLAIIRPPGGVLSI 340

QY 341 SVPGSPGHAMADTYAEQKRGAPAGAGSGTGTGTGARSAPYKVTTPRAQPGAH 400
 DB 341 SVPGSPGHAMADTYAEQKRGAPAGAGSGTGTGTGARSAPYKVTTPRAQPGAH 400

QY 401 AEDARGTLPGRVADQSPAGSGAYEDVAGGAGTGGTGNLRIKRGKGRPPPAETRV 458
 DB 401 AEDARGTLPGRVADQSPAGSGAYEDVAGGAGTGGTGNLRIKRGKGRPPPAETRV 458

RESULT 2
 ADC99051 standard; protein; 353 AA.

XX
 AC ADC99051;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human KPP protein - SEQ ID 4.

XX anti-HIV; anti-allergic; anti-inflammatory; antianaemic; antiparkinsonian;
 XX neurotropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
 XX immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
 XX antidiabetic; nephrotropic; antigout; thyromimetic; neuroprotective;
 XX osteopathic; antiarthritic; antiparasitic; antihelminthic; antiposoriatic;
 XX uropathic; ophthalmologic; antirheumatic; haemostatic; antibacterial;
 XX virucide; protozoacide; fungicide; kinase; phosphatase; KPP;
 XX cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
 XX cancer; developmental; mental retardation; neurological;
 XX Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
 XX diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
 XX helminthic infection; transgenic; gene therapy; human; enzyme.

XX Homo sapiens.
 XX
 XX WO2003033680-A2.
 XX
 XX 24-APR-2003.
 XX
 XX 17-OCT-2002; 2002WO-US033723.
 XX
 XX 19-OCT-2001; 2001US-0345474P.
 XX
 XX 02-NOV-2001; 2001US-0343910P.

PR 13-NOV-2001; 2001US-0333098P.
 PR 16-NOV-2001; 2001US-0332424P.
 PR 30-NOV-2001; 2001US-0334288P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 XX Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
 XX Emerling EM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
 XX Gururajan R, Hafalia AJA, Khan PA, Lal PG, Lee EA, Lee SY;
 XX Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
 XX Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YI;
 XX Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
 XX Zebarjadian Y;
 XX WPI: 2003-403214/38.
 XX N-PSDB; ADC99103.
 XX
 XX New human kinases and phosphatases and polynucleotides, useful for
 XX diagnosing, treating or preventing autoimmune or inflammatory disorders
 XX (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
 XX cancer or hepatitis.
 XX
 XX Claim 1; SEQ ID NO 4; 424pp; English.
 XX
 XX The invention relates to a novel isolated polypeptide which is a human
 XX kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
 XX agonists and antagonists are useful for diagnosing, treating or
 XX preventing cell proliferative disorders such as atherosclerosis,
 XX cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
 XX retardation, neurological disorders including Alzheimer's disease and
 XX Parkinson's disease, autoimmune and inflammatory disorders such as
 XX Crohn's disease and diabetes mellitus and finally, viral, bacterial,
 XX fungal, parasitic, protozoan or helminthic infections. Furthermore, the
 XX polynucleotides encoding KPP may be useful for creating transgenic
 XX animals to model human disease, as well as during gene therapy
 XX procedures. The current sequence is that of the human KPP protein of the
 XX invention.
 XX
 XX Sequence 353 AA;

Query Match 47.4%; Score 217; DB 7; Length 353;
 Best Local Similarity 100.0%; Pred. No. 1.5e-203;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 KRCERYWAOEPLQTLFCITLKEKWLNEIDIMLRTLVKVTFOKESRVYQYMSWPD 198
 DB 32 KRCERYWAOEPLQTLFCITLKEKWLNEIDIMLRTLVKVTFOKESRVYQYMSWPD 91

QY 199 GVPSSPDHMLAVVEARLQSGPEPLCVHCSAGCGRTGVLTVDVYVROLITQMIIPDF 258
 DB 92 GVPSSPDHMLAVVEARLQSGPEPLCVHCSAGCGRTGVLTVDVYVROLITQMIIPDF 151

QY 259 SLFDVVLKMKRQPAVQTEQYRFLVHTVQMFCTLQNASPHYQIKENCAPLYDDAL 318
 DB 152 SLFDVVLKMKRQPAVQTEQYRFLVHTVQMFCTLQNASPHYQIKENCAPLYDDAL 211

QY 319 FLRTQALLAIIRPPGGVLSISVPGSPGHAMADTYA 355
 DB 212 FLRTQALLAIIRPPGGVLSISVPGSPGHAMADTYA 248

RESULT 3
 AAW37255 standard; protein; 155 AA.
 XX
 XX AAW37255;
 XX
 XX 09-APR-1998 (first entry)
 XX
 XX Partial human non-receptor tyrosine phosphatase.
 XX
 XX Non-receptor protein tyrosine phosphatase; hematopoietic stem cell;
 XX PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist;

KW tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist;
 KW stem cell differentiation.
 XX Homo sapiens.
 OS WO9735019-A1.
 PN 25-SEP-1997.
 PD 17-MAR-1997; 97WO-US005278.
 PF 22-MAR-1996; 96US-00620526.
 PR (GETH) GENENTECH INC.
 XX Lasky LA, Cheng J;
 XX WPI; 1997-480224/44.
 DR N-PSDB; AAV03128.
 XX Haematopoietic stem cell non-receptor protein tyrosine phosphatase -
 PT useful for expansion of undifferentiated stem cells in cell culture.
 FT
 PS Claim 9; Fig 8; 66pp; English.
 XX
 CC The present sequence represents a partial human non-receptor protein
 CC tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein
 CC is predominantly expressed in early hematopoietic stem cells (HSCs) or
 CC progenitor cells, and lacks expression in adult tissues. The protein has
 CC a N-terminal tyrosine phosphatase domain, followed by a region rich in
 CC serine, threonine and proline and a C-terminal region of about 15-25
 CC amino acids which is rich in basic amino acid residues. The protein is
 CC capable of tyrosine dephosphorylation in hematopoietic progenitor cells,
 CC and functional derivatives of such native tyrosine phosphatases. The
 CC phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or
 CC progenitor cell can be used in an assay for the identification of PTP HSC
 CC antagonists or agonists. The antagonist can be used to induce the
 CC differentiation of stem cells, such as undifferentiated malignant
 CC hematopoietic cells, e.g. leukaemia cells, which may facilitate their
 CC treatment. The PTP HSC or an agonist antibody against the PTP HSC can be
 CC used for the expansion of undifferentiated stem cells in cell culture
 CC (this allows expansion of HSC prior to autologous or heterologous bone
 CC marrow transplantation), while the agonist antibody along with a
 CC hematopoietic growth factor can be used for the expansion of
 CC undifferentiated stem cells in vivo
 XX
 SQ Sequence 155 AA;
 Query Match 33.8%; Score 155; DB 2; Length 155;
 Best Local Similarity 100.0%; Pred. No. 3.9e-143;
 Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 ARGREGAVLAGFSDIQASAAWKADGVCSWAGSRPENVRNRYKDVLPYDQTRVILS 76
 DB 1 ARGREGAVLAGFSDIQASAAWKADGVCSWAGSRPENVRNRYKDVLPYDQTRVILS 60
 QY 77 LLOEGHSDYNGNFIRGVDGSLAYATQGPLPHTLLDFWRLVWVEFGVKVILMACREIN 136
 DB 61 LLOEGHSDYNGNFIRGVDGSLAYATQGPLPHTLLDFWRLVWVEFGVKVILMACREIN 120
 QY 137 GRKRCERYWAQEPLOTGLFCITLKEKWLNEDI 171
 DB 121 GRKRCERYWAQEPLOTGLFCITLKEKWLNEDI 155
 RESULT 4
 AAW37254
 ID AAW37254 standard; protein; 453 AA.
 XX
 AC AAW37254;
 XX 09-APR-1998 (first entry)
 DT
 XX

DE Novel non-receptor tyrosine phosphatase of hematopoietic stem cells.
 XX
 KW Non-receptor protein tyrosine phosphatase; hematopoietic stem cell;
 KW PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist;
 KW tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist;
 KW stem cell differentiation.
 XX
 OS Mus sp.
 XX
 FH Key Location/Qualifiers
 FT Domain 6..303
 FT Active-site 37
 FT /note= "tyrosine phosphatase domain"
 FT /note= "phosphorylated by protein kinases A and C; also
 FT appears to negatively regulate PTPase activity"
 FT Active-site 229
 FT /note= "active site cysteine residue"
 FT Region 312..428
 FT /note= "pro, Ser and Thr rich region"
 FT Region 430..450
 FT /note= "homologous to a nuclear localization signal found
 FT on murine PTP PEP"
 XX
 PN WO9735019-A1.
 XX 25-SEP-1997.
 PD 17-MAR-1997; 97WO-US005278.
 PF 22-MAR-1996; 96US-00620526.
 PR (GETH) GENENTECH INC.
 XX Lasky LA, Cheng J;
 XX WPI; 1997-480224/44.
 DR N-PSDB; AAV03112.
 XX Haematopoietic stem cell non-receptor protein tyrosine phosphatase -
 PT useful for expansion of undifferentiated stem cells in cell culture.
 FT
 PS Claim 9; Fig 1; 66pp; English.
 XX
 CC The present sequence represents a novel murine non-receptor protein
 CC tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein
 CC is predominantly expressed in early hematopoietic stem cells (HSCs) or
 CC progenitor cells, and lacks expression in adult tissues. The protein has
 CC a N-terminal tyrosine phosphatase domain, followed by a region rich in
 CC serine, threonine and proline and a C-terminal region of about 15-25
 CC amino acids which is rich in basic amino acid residues. The protein is
 CC capable of tyrosine dephosphorylation in hematopoietic progenitor cells,
 CC and functional derivatives of such native tyrosine phosphatases. The
 CC phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or
 CC progenitor cell can be used in an assay for the identification of PTP HSC
 CC antagonists or agonists. The antagonist can be used to induce the
 CC differentiation of stem cells, such as undifferentiated malignant
 CC hematopoietic cells, e.g. leukaemia cells, which may facilitate their
 CC treatment. The PTP HSC or an agonist antibody against the PTP HSC can be
 CC used for the expansion of undifferentiated stem cells in cell culture
 CC (this allows expansion of HSC prior to autologous or heterologous bone
 CC marrow transplantation), while the agonist antibody along with a
 CC hematopoietic growth factor can be used for the expansion of
 CC undifferentiated stem cells in vivo
 XX
 SQ Sequence 453 AA;
 Query Match 7.0%; Score 32; DB 2; Length 453;
 Best Local Similarity 100.0%; Pred. No. 3.1e-22;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 100 AYIATQGPLPHTLLDFWRLVWVEFGVKVILMAC 131
 DB 100 AYIATQGPLPHTLLDFWRLVWVEFGVKVILMAC 131

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RESULT 5
AAW49906
ID AAW49906 standard; protein; 453 AA.
XX AC AAW49906;
XX DT 24-NOV-1998 (first entry)
XX DE Protein tyrosine phosphatase peptide PTP HSCF.
XX KW Mouse; tyrosine phosphorylated cleavage furrow-associated protein;
XX KW PSTPIP; PST family; protein tyrosine phosphatase; murine;
XX KW polymerisation; actin monomer; eukaryotic cell; identification;
XX KW antagonist.
XX OS Synthetic.
XX OS Mus sp.
XX PN WO9835037-A1.
XX PD 13-AUG-1998.
XX PF 30-JAN-1998; 98WO-US001774.
XX PR 07-FEB-1997; 97US-00798419.
XX PR 29-SEP-1997; 97US-00938829.
XX PA (GETH ) GENENTECH INC.
XX PI Laaky LA, Dowbenko DJ;
XX PI MPI; 1998-447234/38.
XX DR
XX PT New PEST-type protein tyrosine phosphatase interacting polypeptide -
XX PT nucleic acids and vectors, for inducing the polymerisation of actin
XX PT monomers in eukaryotic cells and identifying antagonists.
XX PS Disclosure; Page 37; 111pp; English.
XX CC The present sequence represents a peptide from the present invention
XX CC which describes murine tyrosine phosphorylated cleavage furrow-
XX CC associated protein (PSTPIP), which is a PST-type protein tyrosine
XX CC phosphatase (PTP)-interacting polypeptide. PSTPIP induces the
XX CC polymerisation of actin monomers in a eukaryotic cell, by introducing a
XX CC vector containing the nucleic acid sequence encoding PSTPIP into the
XX CC cell. Assays for identifying (ant)agonists of PSTPIP comprise contacting
XX CC PSTPIP with the agent and monitoring the ability of PSTPIP to induce
XX CC actin polymerisation
XX SQ Sequence 20 AA;
Query Match 4.4%; Score 20; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 437 GFNLIRGRPKGRPPPAEWT 456
DB 1 GFNLIRGRPKGRPPPAEWT 20
RESULT 7
AAW81930
ID AAW81930 standard; protein; 20 AA.
XX AC AAW81930;
XX DT 27-JUN-2000 (first entry)
XX DE Peptide fragment of PXXP-HSCF.
XX KW PST phosphatase interacting protein; PSTPIP; tumour therapy;
XX KW protein tyrosine phosphatase; PTP.
XX OS Unidentified.
XX PN US6040437-A.
XX

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RESULT 6
AAW71596
ID AAW71596 standard; peptide; 20 AA.
XX AC AAW71596;
XX DT 24-NOV-1998 (first entry)
XX DE Protein tyrosine phosphatase peptide PTP HSCF.
XX KW Mouse; tyrosine phosphorylated cleavage furrow-associated protein;
XX KW PSTPIP; PST family; protein tyrosine phosphatase; murine;
XX KW polymerisation; actin monomer; eukaryotic cell; identification;
XX KW antagonist.
XX OS Synthetic.
XX OS Mus sp.
XX PN WO9835037-A1.
XX PD 13-AUG-1998.
XX PF 30-JAN-1998; 98WO-US001774.
XX PR 07-FEB-1997; 97US-00798419.
XX PR 29-SEP-1997; 97US-00938829.
XX PA (GETH ) GENENTECH INC.
XX PI Laaky LA, Dowbenko DJ;
XX PI MPI; 1998-447234/38.
XX DR
XX PT New PEST-type protein tyrosine phosphatase interacting polypeptide -
XX PT nucleic acids and vectors, for inducing the polymerisation of actin
XX PT monomers in eukaryotic cells and identifying antagonists.
XX PS Disclosure; Page 37; 111pp; English.
XX CC The present sequence represents a peptide from the present invention
XX CC which describes murine tyrosine phosphorylated cleavage furrow-
XX CC associated protein (PSTPIP), which is a PST-type protein tyrosine
XX CC phosphatase (PTP)-interacting polypeptide. PSTPIP induces the
XX CC polymerisation of actin monomers in a eukaryotic cell, by introducing a
XX CC vector containing the nucleic acid sequence encoding PSTPIP into the
XX CC cell. Assays for identifying (ant)agonists of PSTPIP comprise contacting
XX CC PSTPIP with the agent and monitoring the ability of PSTPIP to induce
XX CC actin polymerisation
XX SQ Sequence 20 AA;
Query Match 6.3%; Score 29; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 430 GAQTGGLGFNLIRGRPKGRPPPAEWT 458
DB 425 GAQTGGLGFNLIRGRPKGRPPPAEWT 453
RESULT 6
AAW71596
ID AAW71596 standard; peptide; 20 AA.
XX AC AAW71596;
XX DT 24-NOV-1998 (first entry)
XX DE Protein tyrosine phosphatase peptide PTP HSCF.
XX KW Mouse; tyrosine phosphorylated cleavage furrow-associated protein;
XX KW PSTPIP; PST family; protein tyrosine phosphatase; murine;
XX KW polymerisation; actin monomer; eukaryotic cell; identification;
XX KW antagonist.
XX OS Synthetic.
XX OS Mus sp.
XX PN WO9835037-A1.
XX PD 13-AUG-1998.
XX PF 30-JAN-1998; 98WO-US001774.
XX PR 07-FEB-1997; 97US-00798419.
XX PR 29-SEP-1997; 97US-00938829.
XX PA (GETH ) GENENTECH INC.
XX PI Laaky LA, Dowbenko DJ;
XX PI MPI; 1998-447234/38.
XX DR
XX PT New PEST-type protein tyrosine phosphatase interacting polypeptide -
XX PT nucleic acids and vectors, for inducing the polymerisation of actin
XX PT monomers in eukaryotic cells and identifying antagonists.
XX PS Disclosure; Page 37; 111pp; English.
XX CC The present sequence represents a novel rat protein tyrosine phosphatase,
XX CC designated PRP20, that regulates growth factor stimulation of cellular
XX CC differentiation. Its amino acid sequence was deduced from a cDNA clone
XX CC (see AAV17097) isolated from a rat phaeochromocytoma PC12 cDNA library by
XX CC PCR amplification using primers based on consensus sequences (see
XX CC AAW49915-16) of known PTPs. The invention relates to novel proteins (see
XX CC AAW49906-14) involved in cellular signal transduction and to the nucleic
XX CC acids (see AAV17097-99) coding for them, and provides vectors, host
XX CC cells, purified recombinant proteins, methods for identifying compounds
XX CC activate or inhibit the novel proteins, as well as methods for the
XX CC diagnosis and treatment of diseases associated with the novel proteins.
XX CC For PRP20, activators may act as anti-cancer therapeutics that stimulate
XX CC cell differentiation rather than proliferation, while inhibitors may be
XX CC useful for treating neural injuries by delaying the differentiation of
XX CC transplanted neuronal stem cells until they are firmly grafted
XX SQ Sequence 453 AA;
Query Match 6.3%; Score 29; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 430 GAQTGGLGFNLIRGRPKGRPPPAEWT 458
DB 425 GAQTGGLGFNLIRGRPKGRPPPAEWT 453
RESULT 6
AAW71596
ID AAW71596 standard; peptide; 20 AA.
XX AC AAW71596;
XX DT 24-NOV-1998 (first entry)
XX DE Protein tyrosine phosphatase peptide PTP HSCF.
XX KW Mouse; tyrosine phosphorylated cleavage furrow-associated protein;
XX KW PSTPIP; PST family; protein tyrosine phosphatase; murine;
XX KW polymerisation; actin monomer; eukaryotic cell; identification;
XX KW antagonist.
XX OS Synthetic.
XX OS Mus sp.
XX PN WO9835037-A1.
XX PD 13-AUG-1998.
XX PF 30-JAN-1998; 98WO-US001774.
XX PR 07-FEB-1997; 97US-00798419.
XX PR 29-SEP-1997; 97US-00938829.
XX PA (GETH ) GENENTECH INC.
XX PI Laaky LA, Dowbenko DJ;
XX PI MPI; 1998-447234/38.
XX DR
XX PT New PEST-type protein tyrosine phosphatase interacting polypeptide -
XX PT nucleic acids and vectors, for inducing the polymerisation of actin
XX PT monomers in eukaryotic cells and identifying antagonists.
XX PS Disclosure; Page 37; 111pp; English.
XX CC The present sequence represents a novel rat protein tyrosine phosphatase,
XX CC designated PRP20, that regulates growth factor stimulation of cellular
XX CC differentiation. Its amino acid sequence was deduced from a cDNA clone
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XX CC PCR amplification using primers based on consensus sequences (see
XX CC AAW49915-16) of known PTPs. The invention relates to novel proteins (see
XX CC AAW49906-14) involved in cellular signal transduction and to the nucleic
XX CC acids (see AAV17097-99) coding for them, and provides vectors, host
XX CC cells, purified recombinant proteins, methods for identifying compounds
XX CC activate or inhibit the novel proteins, as well as methods for the
XX CC diagnosis and treatment of diseases associated with the novel proteins.
XX CC For PRP20, activators may act as anti-cancer therapeutics that stimulate
XX CC cell differentiation rather than proliferation, while inhibitors may be
XX CC useful for treating neural injuries by delaying the differentiation of
XX CC transplanted neuronal stem cells until they are firmly grafted
XX SQ Sequence 453 AA;
Query Match 6.3%; Score 29; DB 2; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.7e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 430 GAQTGGLGFNLIRGRPKGRPPPAEWT 458
DB 425 GAQTGGLGFNLIRGRPKGRPPPAEWT 453

```


PD 21-MAR-2000.
 XX
 PF 29-SEP-1997; 97US-00938830.
 XX
 PR 17-APR-1997; 97US-0104590P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Dowbenko DJ, Lasky LA;
 XX
 DR WPI; 2000-282393/24.
 XX
 PT Novel genes encoding protein tyrosine phosphatase binding proteins useful
 PT for isolating homologous genes, e.g. in tumor cells, which provide more
 PT specific targets for tumor therapy.
 XX
 PS Disclosure; Col 35; 65pp; English.
 XX
 CC This sequence represents a fragment of a protein tyrosine phosphatase
 CC (PTP). It was used to isolate the PTP phosphatase interacting protein
 CC (PSTPIP) sequence of the invention. The protein is a protein tyrosine
 CC phosphatase that possesses a non-catalytic domain comprising a proline,
 CC serine and threonine rich region and a C-terminal segment of 20 amino
 CC acid (aa's) rich in proline, and defines an SH3 binding domain. Nucleic
 CC acids encoding native PSTPIP molecules can be used to isolate homologous
 CC genes specifically expressed in tumour cells, which might provide more
 CC specific targets for tumour therapy. The DNA is also useful for the
 CC preparation of PSTPIP polypeptides by recombinant techniques and as
 CC hybridisation probes for searching cDNA and genomic libraries for the
 CC coding sequence of other PSTPIP polypeptide analogues in other species
 XX
 SQ Sequence 20 AA;
 Query Match 4.4%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 437 GFNLIRGPKGRDPPAEWT 456
 Db 1 GFNLIRGPKGRDPPAEWT 20
 RESULT 8
 AAB08487
 ID AAB08487 standard; peptide; 20 AA.
 AC AAB08487;
 DT 20-DEC-2000 (first entry)
 DE Peptide derived from a protein tyrosine phosphatase.
 KW protein tyrosine phosphatase; PTP; phosphatase interacting protein;
 KW PSTPIP; PEST family; protein tyrosine phosphatase; actin monomer;
 KW tissue typing; tumour cell; tumour imaging.
 XX
 OS Synthetic.
 XX
 XX US6111073-A.
 XX
 XX 29-AUG-2000.
 XX
 XX 06-FEB-1998; 98US-00020222.
 XX
 XX 17-APR-1997; 97US-0104590P.
 XX
 XX (GETH) GENENTECH INC.
 XX
 XX Lasky LA;
 PI
 XX WPI; 2000-586378/55.
 DR
 XX Novel PST phosphatase interacting protein useful for inducing

PT polymerization of actin monomers and for identifying homolog of PST
 XX phosphatase interacting protein.
 PS Disclosure; Col 34; 48pp; English.
 XX
 CC AAB08487-90 represent peptides derived from protein tyrosine phosphatase
 CC (PTP). They were used to identify interaction domains of a murine protein
 CC tyrosine phosphatase (PTP) phosphatase interacting protein (PSTPIP).
 CC PSTPIP polypeptides are bound by and dephosphorylated by the PEST family
 CC of protein tyrosine phosphatases. PSTPIP associates with actin. PSTPIP is
 CC useful for inducing the polymerisation of actin monomer in eukaryotic
 CC cells by introducing the polypeptide into the cell. The polypeptide is
 CC useful for identifying and isolating PSTPIP homologues in another
 CC mammalian species, in screening assays to identify antagonists and
 CC agonists of native PSTPIP polypeptide and as molecular weight markers on
 CC protein gels. The PSTPIP nucleic acid is useful for tissue typing of
 CC specific mammalian tissues, for preparing PSTPIP polypeptides by
 CC recombinant techniques, as hybridisation probes for searching cDNA and
 CC genomic libraries for the coding sequence of other PSTPIP analogues and
 CC to isolate homologous genes specifically expressed in tumour cells.
 CC Antagonists of PSTPIP peptide are useful for inhibiting biological
 CC activity of the peptide. Antibodies of PSTPIP are useful to identify
 CC rapidly dividing cells and are used to image tumours comprising such
 XX rapidly dividing cells
 XX Sequence 20 AA;
 Query Match 4.4%; Score 20; DB 3; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 437 GFNLIRGPKGRDPPAEWT 456
 Db 1 GFNLIRGPKGRDPPAEWT 20
 RESULT 9
 AAB07829
 ID AAB07829 standard; protein; 64 AA.
 XX
 AC AAB07829;
 XX
 DT 24-JUN-2002 (first entry)
 DE Human ORFX protein sequence SEQ ID NO:15640.
 XX
 KW Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.
 XX
 OS Homo sapiens.
 XX
 XX WO200192523-A2.
 XX
 PD 06-DEC-2001.
 XX
 XX 29-MAY-2001; 2001WO-US010836.
 PF
 XX 30-MAY-2000; 2000US-0206132P.
 PR
 XX 29-AUG-2000; 2000US-0228716P.
 XX
 XX (CURA-) CURAGEN CORP.
 PA
 XX Shinkets RA, Leach MD;
 PI
 XX WPI; 2002-106309/14.
 DR
 XX N-PSDB; ABN23581.
 DR
 XX

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VHCAGCGRTG 237
 |||||
 Db 225 VHCAGCGRTG 235

RESULT 14
 AAY28653
 ID AAY28653 standard; protein; 692 AA.
 XX
 AC AAY28653;
 XX
 DT 01-OCT-1999 (first entry)
 XX
 DE Human Cytoplasmic phosphatase, Lyp2 protein.
 XX
 KW Lymphoid Protein Tyrosine Phosphatase; Lyp protein; immunosuppressant;
 KW intracellular tyrosine phosphatase; PTase; fetal liver; transplant;
 KW resting lymphoid cell; protein tyrosine kinase; PKs; lymphocyte;
 KW T cell antigen receptor signalling; cytokine receptor signalling;
 KW autoimmune disease; intronic sequence; alternative mRNA splicing.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 27..289
 FT /label=PTase domain
 FT /note="Single catalytic protein tyrosine phosphatase
 FT domain"
 FT Domain 469..472
 FT /label=NXXY motif
 FT /note="Unique sequence recognised by phosphotyrosine
 FT binding (PTB) domain"
 FT Binding-site 615..623
 FT /label=SH3 binding site
 FT /note="Proline rich sequence"
 XX
 PN WO9936548-A1.
 XX
 PD 22-JUL-1999.
 XX
 PF 18-JAN-1999; 99WO-CA000038.
 XX
 PR 16-JAN-1998; 98CA-02220853.
 XX
 PA (HSCR-) HSC RES & DEV LP.
 XX
 PI Roifman CW;
 XX
 DR WPI; 1999-444404/37.
 DR N-PSDB; AAX90696.
 XX
 PT New nucleic acid encoding intracellular tyrosine phosphatase and related
 PT proteins, used to modulate signaling through T cells, particularly as
 PT immunosuppressant.
 XX
 PS Claim 4b; Page 55; 105pp; English.
 XX
 CC The present protein sequence is that of the cytoplasmic, Lymphoid Protein
 CC Tyrosine Phosphatase, Lyp2 protein that has a single catalytic domain.
 CC The non-catalytic portion of the phosphatase contains unique sequences,
 CC including a single PEST sequence rich in Pro, Glu or Asp, Ser and Thr. It
 CC is expressed significantly in fetal liver and in resting lymphoid cells.
 CC Lyp2 is an isoform of the Lyp1 gene that arises by alternative splicing
 CC of the mRNA. The intronic sequence of Lyp1 encodes for the C-terminal 7
 CC aminoacids and part of the 3'untranslated region of Lyp2. Lyp2 shares
 CC sequence identity with the murine phosphatase Z70PEP. Lyp proteins are
 CC important for regulation of T cell antigen and cytokine receptor
 CC signalling and for early and late stages of T cell differentiation. Lyp2
 CC has immunosuppressive activity. Compounds that increase expression of Lyp
 CC protein can be used as immunosuppressive agents to reduce or prevent T
 CC cell activation or proliferation, to control thymocyte differentiation,

CC to treat autoimmune diseases and transplant situations

XX
 SQ Sequence 692 AA;
 Query Match 2.4%; Score 11; DB 2; Length 692;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 HCSAGCGRTGV 238
 |||||
 Db 226 HCSAGCGRTGV 236

RESULT 15
 AAG78623
 ID AAG78623 standard; protein; 799 AA.
 XX
 AC AAG78623;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE Human tyrosine phosphatase.
 XX
 KW Human; tyrosine phosphatase; hPTP.
 XX
 OS Homo sapiens.
 XX
 PN CN1302899-A.
 XX
 PD 11-JUL-2001.
 XX
 PF 29-OCT-1999; 99CN-00119935.
 XX
 PR 29-OCT-1999; 99CN-00119935.
 XX
 PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.
 XX
 PI Ren S, Wu T, Qian B;
 XX
 DR WPI; 2001-550591/62.
 DR N-PSDB; AAX79342.
 XX
 PT Human protein tyrosine phosphatase and its coding sequence.
 XX
 PS Claim 4; Page 12-13 (Disclosure); 29pp; Chinese.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC tyrosine phosphatase hPTP. The protein is expressed in human normal
 CC suprarenal tissue. The present sequence is the protein of the invention

XX
 SQ Sequence 799 AA;
 Query Match 2.4%; Score 11; DB 4; Length 799;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 HCSAGCGRTGV 238
 |||||
 Db 226 HCSAGCGRTGV 236

Search completed: August 17, 2004, 20:51:35
 Job time : 57 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:50:37 ; Search time 20 Seconds
(without alignments)
1182.235 Million cell updates/sec

Title: US-10-087-993A-36
Perfect score: 458
Sequence: 1 MSRLSARSFLERLEARGG.....NLRIKPKGRDPPAETWTRV 458

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 389414 seqs, 51625971 residues

Word size : 0

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	155	33.8	155	3	US-08-821-278A-17
2	32	7.0	453	3	US-08-821-278A-2
3	29	6.3	453	3	US-08-951-260A-7
4	29	6.3	453	4	US-09-430-626A-7
5	20	4.4	20	3	US-08-938-830-20
6	20	4.4	20	3	US-09-020-222-20
7	11	2.4	231	2	US-08-446-345-37
8	11	2.4	242	2	US-08-685-922-21
9	11	2.4	242	2	US-08-144-925-21
10	11	2.4	244	4	US-09-848-294-7
11	11	2.4	278	3	US-08-821-278A-18
12	11	2.4	802	3	US-09-081-345-18
13	11	2.4	807	3	US-09-081-345-2
14	11	2.4	913	4	US-08-848-294-2
15	10	2.2	20	3	US-08-938-830-23
16	10	2.2	20	3	US-09-020-222-23
17	10	2.2	127	4	US-08-811-481-5
18	10	2.2	127	4	US-08-876-527-5
19	10	2.2	246	4	US-08-884-569A-3
20	10	2.2	250	2	US-08-685-992-7
21	10	2.2	250	2	US-08-144-925-7
22	10	2.2	253	2	US-08-685-992-20
23	10	2.2	253	2	US-08-144-925-20
24	10	2.2	272	3	US-08-821-278A-19
25	10	2.2	289	1	US-08-036-210-13
26	10	2.2	289	2	US-08-449-609-13
27	10	2.2	289	4	US-09-361-096A-13

28 10 2.2 298 4 US-08-811-481-4 Sequence 4, Appli
29 10 2.2 298 4 US-08-876-527-4 Sequence 4, Appli
30 10 2.2 376 4 US-08-811-481-7 Sequence 7, Appli
31 10 2.2 376 4 US-08-876-527-7 Sequence 7, Appli
32 10 2.2 641 4 US-08-811-481-2 Sequence 2, Appli
33 10 2.2 641 4 US-08-876-527-2 Sequence 2, Appli
34 10 2.2 723 2 US-08-548-159-5 Sequence 5, Appli
35 10 2.2 818 4 US-08-811-481-22 Sequence 22, Appli
36 10 2.2 818 4 US-08-876-527-22 Sequence 22, Appli
37 10 2.2 969 2 US-08-548-159-1 Sequence 1, Appli
38 10 2.2 986 2 US-08-548-159-3 Sequence 3, Appli
39 10 2.2 1001 4 US-08-884-569A-2 Sequence 2, Appli
40 10 2.2 1012 4 US-08-811-481-16 Sequence 16, Appli
41 10 2.2 1012 4 US-08-876-527-16 Sequence 16, Appli
42 10 2.2 1501 2 US-08-447-454-3 Sequence 3, Appli
43 10 2.2 1501 2 US-08-716-679-3 Sequence 3, Appli
44 10 2.2 1911 1 US-08-348-006B-5 Sequence 5, Appli
45 10 2.2 1911 2 US-08-800-825A-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-821-278A-17
; Sequence 17, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 17
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo Sapien
US-08-821-278A-17

Query Match 33.8%; Score 155; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 1.9e-134;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ARGREGAVLAGEFSDIQACSAANKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS 76
Db 1 ARGREGAVLAGEFSDIQACSAANKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILS 60
QY 77 LLOEGHSDYINGNFIKRGVDSGLAVIATCGPLPHTLLDFWRLVWFEFGVKVIMACREIEN 136
Db 61 LLOEGHSDYINGNFIKRGVDSGLAVIATCGPLPHTLLDFWRLVWFEFGVKVIMACREIEN 120
QY 137 GRKRCERYWAQOEPIQTGLFCITLIEKKNLNEDI 171
Db 121 GRKRCERYWAQOEPIQTGLFCITLIEKKNLNEDI 155

RESULT 2
US-08-821-278A-2
; Sequence 2, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 2
; LENGTH: 453
; TYPE: PRT


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; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,830
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/798419
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1066P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-938-830-20

Query Match 4.4%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.5e-11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 437 GFNLRIGRPKGRDPPPAEWT 456
DB 1 GFNLRIGRPKGRDPPPAEWT 20

RESULT 7
US-08-446-345-37
; Sequence 37, Application US/08446345
; Patent No. 5831009
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; APPLICANT: Moller, Niels P.H.
; APPLICANT: Moller, Karin B.
; TITLE OF INVENTION: NOVEL PROTEIN PHOSPHOTYROSINE
; TITLE OF INVENTION: PHOSPHATASES PTP-D1
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: N.Y.
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,345
; FILING DATE: 22-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/234,440
; FILING DATE: 28-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30742
; REFERENCE/DOCKET NUMBER: 7683-054
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 231 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-446-345-37

Query Match 2.4%; Score 11; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KRYKQVLPYD 69
DB 4 KRYKQVLPYD 14

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RESULT 8
US-08-685-992-21
; Sequence 21, Application US/08685992
; Patent No. 5912138
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/685,992
; FILING DATE: 25-JUL-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-685-992-21
Query Match 2.4%; Score 11; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KRYKDVLPYD 69
Db 15 KRYKDVLPYD 25

RESULT 9
US-09-144-925-21
; Sequence 21, Application US/09144925
; Patent No. 5951979
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas
; APPLICANT: Flint, Andrew J.
; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
; TITLE OF INVENTION: TYROSINE PHOSPHATASES
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02421-4799
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,925
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585,992
; FILING DATE: July 25, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: CSHL96-03Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 781-861-6240
; TELEFAX: 781-861-9540
; TELEX:
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-144-925-21
Query Match 2.4%; Score 11; DB 2; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KRYKDVLPYD 69
Db 15 KRYKDVLPYD 25

RESULT 10
US-09-848-294-7
; Sequence 7, Application US/09848294
; Patent No. 6479640
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
; TITLE OF INVENTION: Adhesions and Uses Therefor
; FILE REFERENCE: CSHL90-04FZA
; CURRENT APPLICATION NUMBER: US/09/848,294
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/235,251
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/759,536
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: 08/107,420
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: 07/663,579
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 07/494,036
; PRIOR FILING DATE: 1990-03-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-7
Query Match 2.4%; Score 11; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.044;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KRYKDVLPYD 69
|||||
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```
Db      4 KIRYKVLVPYD 14

RESULT 11
US-08-821-278A-18
; Sequence 18, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821.278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 18
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo Sapien
US-08-821-278A-18

Query Match      2.4%; Score 11; DB 3; Length 278;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      228 HCSAGCGRTGV 238
      |||||||
Db      203 HCSAGCGRTGV 213

RESULT 12
US-09-081-345-18
; Sequence 18, Application US/09081345
; Patent No. 6228641
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; APPLICANT: Gregory D. Plowman
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: PTP04 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081.345
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/047,222
; FILING DATE: May 20, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/253
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 802 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-081-345-18

Query Match      2.4%; Score 11; DB 3; Length 807;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      228 HCSAGCGRTGV 238
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Db      226 HCSAGCGRTGV 236

RESULT 13
US-09-081-345-2
; Sequence 2, Application US/09081345
; Patent No. 6228641
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; APPLICANT: Gregory D. Plowman
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: PTP04 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081.345
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/047,222
; FILING DATE: May 20, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/253
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-081-345-2

Query Match      2.4%; Score 11; DB 3; Length 807;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      228 HCSAGCGRTGV 238
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Db      226 HCSAGCGRTGV 236

RESULT 14
US-09-848-294-2
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; Sequence 2, Application US/09848294
; Patent No. 6479640
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. 6479640el
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
; TITLE OF INVENTION: Adhesions and Uses therefor
; FILE REFERENCE: CSHL90-04FZA
; CURRENT APPLICATION NUMBER: US/09/848,294
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/235,251
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/759,536
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: 08/107,420
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: 07/663,579
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 07/494,036
; PRIOR FILING DATE: 1990-03-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 913
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-2

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Query Match 2.4%; Score 11; DB 4; Length 913;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 59 KRYKQVLPYD 69
Db 673 KRYKQVLPYD 693

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RESULT 15
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; Sequence 23, Application US/08938830
; Patent No. 6040437
; GENERAL INFORMATION:
; APPLICANT: Lasky, Laurence A.
; APPLICANT: Dowbenko, Donald J.
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
; TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPs)
; NUMBER OF SEQUENCES: 73
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,830
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/798419
; FILING DATE: 07-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: F1066P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881

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; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-938-830-23
Query Match 2.2%; Score 10; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 334 GGVLRISISVP 343
Db 1 GGVLRISISVP 10
Search completed: August 17, 2004, 20:56:37
Job time : 21 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 17, 2004, 20:52:38 ; Search time 46 Seconds
(without alignments)
3125.622 Million cell ur

Title: US-10-087-993A-36

perfect score: 458
Sequence: 1 MSRSLDSARSFLERLEARGG.....NLRIGRPKGRDPDPAEWTRV 458

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1292805 seqs, 313927144 residues

Word size :

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 200000000
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Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/pdata/1/pubaa/US07_PUBCOMB.pcp.*
2: /cgn2_6/pdata/1/pubaa/FCI_NEW_PUB.pcp.*
3: /cgn2_6/pdata/1/pubaa/US06_NEW_PUB.pcp.*
4: /cgn2_6/pdata/1/pubaa/US06_PUBCOMB.pcp.*
5: /cgn2_6/pdata/1/pubaa/US07_NEW_PUB.pcp.*
6: /cgn2_6/pdata/1/pubaa/FCIUS_PUBCOMB.pcp.*
7: /cgn2_6/pdata/1/pubaa/US08_NEW_PUB.pcp.*
8: /cgn2_6/pdata/1/pubaa/US08_PUBCOMB.pcp.*
9: /cgn2_6/pdata/1/pubaa/US09_PUBCOMB.pcp.*
10: /cgn2_6/pdata/1/pubaa/US09B_PUBCOMB.pcp.*
11: /cgn2_6/pdata/1/pubaa/US09C_PUBCOMB.pcp.*
12: /cgn2_6/pdata/1/pubaa/US09_NEW_PUB.pcp.*
13: /cgn2_6/pdata/1/pubaa/US10A_PUBCOMB.pcp.*
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15: /cgn2_6/pdata/1/pubaa/US10C_PUBCOMB.pcp.*
16: /cgn2_6/pdata/1/pubaa/US10_NEW_PUB.pcp.*
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19: /cgn2_6/pdata/1/pubaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	458	100.0	458	13	US-10-087-993-36		Sequence 36, Appl
2	29	6.3	453	14	US-10-043-681-7		Sequence 7, Appl
3	24	5.2	448	13	US-10-087-993-32		Sequence 32, Appl
4	20	4.4	20	14	US-10-340-288-13		Sequence 13, Appl
5	12	2.6	750	9	US-09-801-368-280		Sequence 280, App
6	12	2.6	750	15	US-10-369-493-2392		Sequence 2392, A
7	11	2.4	235	12	US-10-087-684-94		Sequence 94, Appl
8	11	2.4	235	12	US-10-218-779-94		Sequence 94, Appl
9	11	2.4	235	12	US-10-072-013-819		Sequence 819, App
10	11	2.4	244	9	US-09-848-394-7		Sequence 7, Appl
11	11	2.4	244	14	US-10-293-231-7		Sequence 7, Appl
12	11	2.4	263	12	US-10-087-684-93		Sequence 93, Appl
13	11	2.4	263	12	US-10-218-779-93		Sequence 93, Appl
14	11	2.4	291	9	US-09-788-626-22		Sequence 22, Appl
15	11	2.4	692	15	US-10-309-423-4		Sequence 4, Appl

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; FILING DATE: June 17, 1996
; APPLICATION NUMBER: U.S. 60/023,485
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: U.S. 60/030,860
; FILING DATE: No. US20020169303A1ember 13, 1996
; APPLICATION NUMBER: U.S. 60/034,286
; FILING DATE: December 19, 1996
; APPLICATION NUMBER: U.S. 60/030,964
; FILING DATE: No. US20020169303A1ember 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 225/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 458 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 36:
US-10-087-993-36

Query Match 100.0%; Score 458; DB 13; Length 458;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSRLSDARSFLERLEARGREGAVLAGESFDIQACSAWKADVCSTVAGSRPENVRKN 60
Db 1 MSRLSDARSFLERLEARGREGAVLAGESFDIQACSAWKADVCSTVAGSRPENVRKN 60

Qy 61 RYKDVLPYDQTRVLSLLQEGHSDYINGNFIQVDSGLAYIATQGPLPHTLLDFWRLVW 120
Db 61 RYKDVLPYDQTRVLSLLQEGHSDYINGNFIQVDSGLAYIATQGPLPHTLLDFWRLVW 120

Qy 121 EFGVKVILMACRIENGRKRCERYWAQEQPLQTLGFCITLKEKWLNEIDMLRTLKVTFF 180
Db 121 EFGVKVILMACRIENGRKRCERYWAQEQPLQTLGFCITLKEKWLNEIDMLRTLKVTFF 180

Qy 181 QKESRSVYQLQYMSWDRGVPSPDHMLAMVEARLQSGPPLCVHCSAGCGRTGVLC 240
Db 181 QKESRSVYQLQYMSWDRGVPSPDHMLAMVEARLQSGPPLCVHCSAGCGRTGVLC 240

Qy 241 TVDYVROLTLTQMPDPFSLFDVVLKMKRKPAAVQTESQYRFLYHTVAQMFCSLTQNAS 300
Db 241 TVDYVROLTLTQMPDPFSLFDVVLKMKRKPAAVQTESQYRFLYHTVAQMFCSLTQNAS 300

Qy 301 PHYQNIKENCAPLYDDALFRTQALLAIPRPFGVLRISVPGSPCHAMADTYAEQKR 360
Db 301 PHYQNIKENCAPLYDDALFRTQALLAIPRPFGVLRISVPGSPCHAMADTYAEQKR 360

Qy 361 GAPAGAGSGTGTGTGARGAEEAPLYSKVTTPRAQPGAFADARGTLPGRVPADQSPAG 420
Db 361 GAPAGAGSGTGTGTGARGAEEAPLYSKVTTPRAQPGAFADARGTLPGRVPADQSPAG 420

Qy 421 SGAYEDVAGAGTGGGLGFNLIRIGRPKPRDPPAEWTRV 458
Db 421 SGAYEDVAGAGTGGGLGFNLIRIGRPKPRDPPAEWTRV 458

RESULT 2
US-10-243-687-7
; Sequence 7, Application US/10243687
; Publication No. US20030073120A1
; GENERAL INFORMATION:
; APPLICANT: Aoki, Naohito
; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
; AND RELATED PRODUCTS AND METHODS

```

```

; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/243,687
; FILING DATE: 16-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,626A
; FILING DATE: 29-Oct-1999
; APPLICATION NUMBER: 08/951,260
; FILING DATE: October 16, 1997
; APPLICATION NUMBER: 60/030,860
; FILING DATE: No. US20030073120A1ember 13, 1996
; APPLICATION NUMBER: PCT/1897/00946
; FILING DATE: June 17, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 227/004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-243-687-7

Query Match 6.3%; Score 29; DB 14; Length 453;
Best Local Similarity 100.0%; Pred. No. 4.6e-19;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 430 GAQTGGGLGFNLIRIGRPKPRDPPAEWTRV 458
Db 425 GAQTGGGLGFNLIRIGRPKPRDPPAEWTRV 453

RESULT 3
US-10-087-993-32
; Sequence 32, Application US/10087993
; Publication No. US20020169303A1
; GENERAL INFORMATION:
; APPLICANT: Ullrich, Axel
; Aoki, Naohito
; Kim, Yeong Woong
; Wang, Hong Yang
; Chen, Zhengjun
; Naylor, Oliver
; Kharitonov, Alexei Igorevich
; TITLE OF INVENTION: NOVEL PTP20, PDE-2, BDP1, CLK,
; AND S1RP POLYPEPTIDES AND RELATED
; PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon

```

```
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/087,993
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,150
; FILING DATE: June 17, 1997
; APPLICATION NUMBER: U.S. 60/019,629
; FILING DATE: June 17, 1996
; APPLICATION NUMBER: U.S. 60/023,485
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: U.S. 60/030,860
; FILING DATE: No. US20020169303A1ember 13, 1996
; APPLICATION NUMBER: U.S. 60/034,286
; FILING DATE: December 19, 1996
; APPLICATION NUMBER: U.S. 60/030,964
; FILING DATE: No. US20020169303A1ember 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 225/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
;
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-087-993-32
;
; Query Match 5.2%; Score 24; DB 13; Length 448;
; Best Local Similarity 100.0%; Pred. No. 3.2e-14;
; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Qy 100 AYIATQGPLPHTLLDFWRLVWVFG 123
; Db 100 AYIATQGPLPHTLLDFWRLVWVFG 123
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; RESULT 4
; US-10-340-288-13
; Sequence 13, Application US/10340288
; Publication No. US20030170855A1
; GENERAL INFORMATION:
; APPLICANT: Albert Einstein College of Medicine of Yeshiva University
; APPLICANT: ZHANG, Zhong-Yin
; APPLICANT: XIE, Jiaoping
; APPLICANT: ZHANG, Yan-Ling
; TITLE OF INVENTION: A NOVEL PROTEIN TYROSINE PHOSPHATASE SUBSTRATE-TRAPPING DOUBLE
; FILE OF INVENTION: MUTANT AND USES THEREOF
; FILE REFERENCE: 96700/792
; CURRENT APPLICATION NUMBER: US/10/340,288
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/347,413
; PRIOR FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 37
;
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; STATE: Los Angeles
; COUNTRY: California
; ZIP: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FASTSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/087,993
; FILING DATE: 05-Mar-2002
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/877,150
; FILING DATE: June 17, 1997
; APPLICATION NUMBER: U.S. 60/019,629
; FILING DATE: June 17, 1996
; APPLICATION NUMBER: U.S. 60/023,485
; FILING DATE: August 9, 1996
; APPLICATION NUMBER: U.S. 60/030,860
; FILING DATE: No. US20020169303A1ember 13, 1996
; APPLICATION NUMBER: U.S. 60/034,286
; FILING DATE: December 19, 1996
; APPLICATION NUMBER: U.S. 60/030,964
; FILING DATE: No. US20020169303A1ember 15, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 225/298
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
;
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-087-993-32
;
; Query Match 5.2%; Score 24; DB 13; Length 448;
; Best Local Similarity 100.0%; Pred. No. 3.2e-14;
; Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Qy 100 AYIATQGPLPHTLLDFWRLVWVFG 123
; Db 100 AYIATQGPLPHTLLDFWRLVWVFG 123
;
; RESULT 4
; US-10-340-288-13
; Sequence 13, Application US/10340288
; Publication No. US20030170855A1
; GENERAL INFORMATION:
; APPLICANT: Albert Einstein College of Medicine of Yeshiva University
; APPLICANT: ZHANG, Zhong-Yin
; APPLICANT: XIE, Jiaoping
; APPLICANT: ZHANG, Yan-Ling
; TITLE OF INVENTION: A NOVEL PROTEIN TYROSINE PHOSPHATASE SUBSTRATE-TRAPPING DOUBLE
; FILE OF INVENTION: MUTANT AND USES THEREOF
; FILE REFERENCE: 96700/792
; CURRENT APPLICATION NUMBER: US/10/340,288
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 60/347,413
; PRIOR FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 37
;
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-340-288-13
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; Query Match 4.4%; Score 20; DB 14; Length 20;
; Best Local Similarity 100.0%; Pred. No. 1.4e-11;
; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Qy 263 VVLMKMKQKQRPAAVQTEEQYR 282
; Db 1 VVLMKMKQKQRPAAVQTEEQYR 20
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; RESULT 5
; US-09-801-368-280
; Sequence 280, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 280
; LENGTH: 750
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
; US-09-801-368-280
;
; Query Match 2.6%; Score 12; DB 9; Length 750;
; Best Local Similarity 100.0%; Pred. No. 0.021;
; Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 227 VHCSAGCGRTGV 238
; Db 664 VHCSAGCGRTGV 675
;
; RESULT 6
; US-10-369-493-22392
; Sequence 22392, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
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Query Match 2.6%; Score 12; DB 15; Length 750;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 NUMBER OF SEQ ID NOS: 47374
 SEQ ID NO 22392
 LENGTH: 750
 TYPE: PRT
 ORGANISM: Saccharomyces cerevisiae
 US-10-369-493-22392

Query Match 2.6%; Score 12; DB 15; Length 750;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCAGCGRTGV 238
 Db 664 VHCAGCGRTGV 675

RESULT 7

US-10-087-684-94
 ; Sequence 94, Application US/10087684
 ; Publication No. US20040029116A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edinger, Shlomit R.
 ; APPLICANT: MacDougall, John R.
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Stone, David J.
 ; APPLICANT: Grosse, William M.
 ; APPLICANT: Lepley, Denise M.
 ; APPLICANT: Rieger, Daniel K.
 ; APPLICANT: Burgess, Catherine E.
 ; APPLICANT: Casman, Stacie, J.
 ; APPLICANT: Spytek, Kimberly A.
 ; APPLICANT: Boldog, Ferenc L.
 ; APPLICANT: Li, Li
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Mishra, Vishnu
 ; APPLICANT: Shenoy, Suresh G.
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Tchernev, Velizar T.
 ; APPLICANT: Vernet, Corine A.M.
 ; APPLICANT: Zerhusen, Bryan D.
 ; APPLICANT: Malyankar, Uriel M.
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Miller, Charles E.
 ; APPLICANT: Gargolli, Esha A.
 ; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-214 CIP
 ; CURRENT APPLICATION NUMBER: US/10/087,684
 ; CURRENT FILING DATE: 2003-03-10
 ; PRIOR APPLICATION NUMBER: 60/253,834
 ; PRIOR FILING DATE: 2000-11-29
 ; PRIOR APPLICATION NUMBER: 60/250,926
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: 60/264,180
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 60/274,194
 ; PRIOR FILING DATE: 2001-03-08
 ; PRIOR APPLICATION NUMBER: 60/313,656
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: 60/327,456
 ; PRIOR FILING DATE: 2001-10-05
 ; NUMBER OF SEQ ID NOS: 220
 ; SOFTWARE: CuraSeqlist version 0.1
 ; SEQ ID NO 94
 ; LENGTH: 235
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Domain
 US-10-087-684-94

Query Match 2.4%; Score 11; DB 12; Length 235;
 Best Local Similarity 100.0%; Pred. No. 0.07;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 KORYKDVLPYD 69
 Db 4 KORYKDVLPYD 14

RESULT 8

US-10-218-779-94
 ; Sequence 94, Application US/10218779
 ; Publication No. US20040029222A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Edinger, Shlomit
 ; APPLICANT: MacDougall, John
 ; APPLICANT: Millet, Isabelle
 ; APPLICANT: Ellerman, Karen
 ; APPLICANT: Stone, David
 ; APPLICANT: Gerlach, Valerie
 ; APPLICANT: Grosse, William
 ; APPLICANT: Alsobrook II, John
 ; APPLICANT: Lepley, Denise
 ; APPLICANT: Rieger, Daniel
 ; APPLICANT: Burgess, Catherine
 ; APPLICANT: Casman, Stacie
 ; APPLICANT: Spytek, Kimberly
 ; APPLICANT: Boldog, Ferenc
 ; APPLICANT: Li, Li
 ; APPLICANT: Padigaru, Muralidhara
 ; APPLICANT: Mishra, Vishnu
 ; APPLICANT: Patturajan, Meera
 ; APPLICANT: Shenoy, Suresh
 ; APPLICANT: Rastelli, Luca
 ; APPLICANT: Tchernev, Velizar
 ; APPLICANT: Vernet, Corine
 ; APPLICANT: Zerhusen, Bryan
 ; APPLICANT: Malyankar, Uriel
 ; APPLICANT: Guo, Xiaojia
 ; APPLICANT: Miller, Charles
 ; APPLICANT: Gargolli, Esha
 ; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
 ; FILE REFERENCE: 21402-214
 ; CURRENT APPLICATION NUMBER: US/10/218,779
 ; CURRENT FILING DATE: 2002-08-14
 ; PRIOR APPLICATION NUMBER: 60/253,834
 ; PRIOR FILING DATE: 2000-11-29
 ; PRIOR APPLICATION NUMBER: 60/250,926
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: 60/264,180
 ; PRIOR FILING DATE: 2001-01-25
 ; PRIOR APPLICATION NUMBER: 60/313,656
 ; PRIOR FILING DATE: 2001-08-20
 ; PRIOR APPLICATION NUMBER: 60/327,456
 ; PRIOR FILING DATE: 2001-10-05
 ; NUMBER OF SEQ ID NOS: 216
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 94
 ; LENGTH: 235
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-218-779-94

Query Match 2.4%; Score 11; DB 12; Length 235;
 Best Local Similarity 100.0%; Pred. No. 0.07;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 KORYKDVLPYD 69
 Db 4 KORYKDVLPYD 14

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RESULT 9
US-10-072-012-819
; Sequence 819, Application US/10072012
; Publication No. US20040033493A1
; GENERAL INFORMATION:
; APPLICANT: Tchernev, Velizar
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zethusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Shimkets, Richard
; APPLICANT: Li, Li
; APPLICANT: Gangolli, Esha
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Anderson, David W.
; APPLICANT: Rastelli, Luca
; APPLICANT: Miller, Charles E.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Tsupier Jr, Raymond J.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Colman, Steven D.
; APPLICANT: Wolenc, Adam R.
; APPLICANT: Pena, Carol E. A
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Grosse, William M.
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-258
; CURRENT APPLICATION NUMBER: US/10/072,012
; CURRENT FILING DATE: 2002-01-31
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,102
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/265,514
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,517
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,412
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/265,395
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: 60/266,406
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 60/266,767
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 60/267,057
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/266,975
; PRIOR FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: 60/267,459
; PRIOR FILING DATE: 2001-02-08
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1391
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 819
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Protein-tyrosine phosphatase Consensus Sequence
US-10-072-012-819

Query Match          2.4%; Score 11; DB 12; Length 235;
Best Local Similarity 100.0%; Pred. No. 0.07;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      59 KNRKDVLPYD 69
DB      4 KNRKDVLPYD 14

RESULT 10
US-09-848-294-7
; Sequence 7, Application US/09848294
; Patent No. US20020049179A1
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: Isolation of A cDNA Encoding A No. US20020049179A1el
; TITLE OF INVENTION: Protein Tyrosine Phosphatase Which Localizes to Focal
; TITLE OF INVENTION: Adhesions and Uses Therefor
; FILE REFERENCE: CSHL90-04PZA
; CURRENT APPLICATION NUMBER: US/09/848,294
; CURRENT FILING DATE: 2001-05-03
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 08/759,536
; PRIOR FILING DATE: 1996-12-04
; PRIOR APPLICATION NUMBER: 08/107,420
; PRIOR FILING DATE: 1993-08-16
; PRIOR APPLICATION NUMBER: 07/663,579
; PRIOR FILING DATE: 1991-03-01
; PRIOR APPLICATION NUMBER: 07/494,036
; PRIOR FILING DATE: 1990-03-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homosapiens
US-09-848-294-7

Query Match          2.4%; Score 11; DB 9; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      59 KNRKDVLPYD 69
DB      4 KNRKDVLPYD 14

RESULT 11
US-10-293-231-7
; Sequence 7, Application US/10293231
; Publication No. US20030113294A1
; GENERAL INFORMATION:
; APPLICANT: Tonks, Nicholas K.
; TITLE OF INVENTION: ISOLATION OF A cDNA ENCODING A NOVEL
; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE WHICH LOCALIZES
; TITLE OF INVENTION: TO FOCAL ADHESIONS AND USES THEREOF
; FILE REFERENCE: 200125.409C3
; CURRENT APPLICATION NUMBER: US/10/293,231
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 7
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-231-7

Query Match          2.4%; Score 11; DB 14; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.072;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      59 KNRKDVLPYD 69
DB      4 KNRKDVLPYD 14

RESULT 12
US-10-087-684-93
; Sequence 93, Application US/10087684
; Publication No. US20040029116A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit R.
```

```

; APPLICANT: MacDougall, John R.
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David J.
; APPLICANT: Grosse, William M.
; APPLICANT: Lepley, Denise M.
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie, J.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles E.
; APPLICANT: Gangolli, Esha A.
; TITLE OF INVENTION: PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-214 CIP
; CURRENT APPLICATION NUMBER: US/10/087,684
; CURRENT FILING DATE: 2003-03-10
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/274,194
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 0.1
; SOFTWARE: CuraseqIst version 0.1
; SEQ ID NO 93
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Domain
US-10-087-684-93

Query Match      2.4%; Score 11; DB 12; Length 263;
Best Local Similarity 100.0%; Pred.No. 0.077;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      59 KNRKXDVLPYD 69
Db      30 KNRKXDVLPYD 40

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RESULT 13
US-10-218-779-93
; Sequence 93, Application US/10218779
; Publication No. US2004002222A1
; GENERAL INFORMATION:
; APPLICANT: Edinger, Shlomit
; APPLICANT: MacDougall, John
; APPLICANT: Millet, Isabelle
; APPLICANT: Ellerman, Karen
; APPLICANT: Stone, David
; APPLICANT: Gerlach, Valerie
; APPLICANT: Grosse, William
; APPLICANT: Alsbrook II, John
; APPLICANT: Lepley, Denise
; APPLICANT: Rieger, Daniel

```

```

; APPLICANT: Burgess, Catherine
; APPLICANT: Casman, Stacie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Boldog, Ferenc
; APPLICANT: Li, Li
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Mishra, Vishnu
; APPLICANT: Patturajan, Meera
; APPLICANT: Shenoy, Suresh
; APPLICANT: Rastelli, Luca
; APPLICANT: Tchernev, Velizar
; APPLICANT: Vernet, Corine
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Malyankar, Uriel
; APPLICANT: Guo, Xiaojia
; APPLICANT: Miller, Charles
; APPLICANT: Gangolli, Esha
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-214
; CURRENT APPLICATION NUMBER: US/10/218,779
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 60/253,834
; PRIOR FILING DATE: 2000-11-29
; PRIOR APPLICATION NUMBER: 60/250,926
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/264,180
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/313,656
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/327,456
; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 216
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-218-779-93

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Query Match      2.4%; Score 11; DB 12; Length 263;
Best Local Similarity 100.0%; Pred.No. 0.077;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      59 KNRKXDVLPYD 69
Db      30 KNRKXDVLPYD 40

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RESULT 14
US-09-788-626-22
; Sequence 22, Application US/09788626
; Patent No. US20020009762A1
; GENERAL INFORMATION:
; APPLICANT: Flint, Andrew J.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: IMPROVED ASSAY FOR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATES
; FILE REFERENCE: 200125.401
; CURRENT APPLICATION NUMBER: US/09/788,626
; CURRENT FILING DATE: 2001-02-13
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-788-626-22

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Query Match      2.4%; Score 11; DB 9; Length 291;
Best Local Similarity 100.0%; Pred.No. 0.084;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      59 KNRKXDVLPYD 69

```


Db 15 KRYKDLVLD 25

RESULT 15
US-10-309-423-4
; Sequence 4, Application US/10309423
; Publication No. US20040006777A1
; GENERAL INFORMATION:
; APPLICANT: HSC Research and Development Limited Partnership
; TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases
; FILE REFERENCE: 92906-2
; CURRENT APPLICATION NUMBER: US/10/309,423
; PRIORITY FILING DATE: 2002-12-03
; PRIOR APPLICATION NUMBER: US/09/600,358
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: CA 2,220,853
; PRIOR FILING DATE: 1998-01-16
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 692
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-423-4

Query Match 2.43; Score 11; DB 15; Length 692;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 228 HCSAGCGRTGV 238
Db 226 HCSAGCGRTGV 236

Search completed: August 17, 2004, 20:58:15
Job time : 47 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:49:12 ; Search time 16 Seconds
(without alignments)
2753.482 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 458

Sequence: 1 MRSRLDSARSLERLEARGG.....NLRIGRKGRDPPAEWTRV 458

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283366 seqs, 96191526 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_78.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	12	2.6	750	2 S67100	protein-tyrosine-p
2	11	2.4	303	1 S28392	protein-tyrosine-p
3	11	2.4	802	1 B44390	protein-tyrosine-p
4	11	2.4	913	1 A41109	protein-tyrosine-p
5	11	2.4	928	2 S50578	hypothetical prote
6	11	2.4	1132	2 T49403	related to protein
7	11	2.4	1187	1 JC4155	protein-tyrosine-p
8	11	2.4	1189	1 JC2366	protein-tyrosine-p
9	10	2.2	248	2 T46903	hypothetical prote
10	10	2.2	340	2 T51846	protein-tyrosine-p
11	10	2.2	340	2 C96741	hypothetical prote
12	10	2.2	382	1 S48748	protein-tyrosine-p
13	10	2.2	582	2 A57088	protein-tyrosine-p
14	10	2.2	597	2 B53978	protein-tyrosine-p
15	10	2.2	694	2 A53978	protein-tyrosine-p
16	10	2.2	773	1 JH0609	protein-tyrosine-p
17	10	2.2	775	2 S55345	protein-tyrosine-p
18	10	2.2	780	1 JC1368	protein-tyrosine-p
19	10	2.2	1015	2 JC5283	transmembrane tyro
20	10	2.2	1015	2 JC5082	phogrin precursor
21	10	2.2	1262	1 B48758	protein-tyrosine-p
22	10	2.2	1290	2 A56493	leucocyte common a
23	10	2.2	1437	2 T31093	probable protein-t
24	10	2.2	1496	1 A48758	protein-tyrosine-p
25	10	2.2	1499	2 T50212	protein-tyrosine-p
26	10	2.2	1501	2 T58148	protein-tyrosine-p
27	10	2.2	1863	2 S46217	protein-tyrosine-p
28	10	2.2	1897	1 TDHULK	leukocyte antigen-
29	10	2.2	1898	2 S46216	leukocyte antigen-

RESULT 1

S67100

protein-tyrosine-phosphatase (EC 3.1.3.48) PTP2 - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein O4849; protein YOR208W
C:Species: Saccharomyces cerevisiae
C>Date: 12-Jul-1996 #sequence revision 12-Jul-1996 #text change 21-Jul-2000
C:Accession: S67100; A42667; A41980; S31554; S14170; JCL484; S42155

R;Hughes, B.; Pohl, T.M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S66685

A:Accession: S67100

A:Molecule type: DNA

A:Residues: 1-750 <HUG>

A:Cross-references: EMBL:275116; NID:G1420486; PID:e252394; PID:G1420487; MIPS:YOR208W

A:Experimental source: strain S288C

R;Guan, K.L.; Deschenes, R.J.; Dixon, J.E.

J. Biol. Chem. 267, 10024-10030, 1992

A:Title: Isolation and characterization of a second protein tyrosine phosphatase gene, P1

A:Reference number: A42667; MUID:92250559; PMID:1577774

A:Molecule type: DNA

A:Residues: 1-473, 'NV', 476-750 <GUA>

A:Cross-references: GB:M85287

R;Ota, I.M.; Varshavsky, A.

Proc. Natl. Acad. Sci. U.S.A. 89, 2355-2359, 1992

A:Title: A gene encoding a putative tyrosine phosphatase suppresses lethality of an N-enc

A:Reference number: A41980; MUID:92196117; PMID:1549598

A:Accession: A41980

A:Molecule type: DNA

A:Residues: 1-750 <OTA>

A:Cross-references: EMBL:M82872; NID:G172293; PIDN:AAA34922.1; PID:G172294

A>Note: sequence extracted from NCBI backbone (NCBIN:88405, NCBIP:88407)

R;James, P.; Hall, B.D.; Whelen, S.; Craig, E.A.

submitted to the EMBL Data Library, July 1991

A:Description: Multiple protein tyrosine phosphatase-encoding genes in the yeast Sacchar

A:Reference number: S31554

A:Accession: S31554

A:Molecule type: DNA

A:Residues: 1-370, 'S', 372-659, 'GA', 662-750 <JAM>

A:Cross-references: EMBL:M38723; NID:G172381; PID:G172382

R;James, P.; Whelen, S.; Hall, B.D.

J. Biol. Chem. 266, 5616-5624, 1991

A:Title: The RFI1 gene of yeast encodes the second-largest subunit of RNA polymerase III

A:Reference number: S14170; MUID:91170230; PMID:2005101

A:Accession: S14170

A:Molecule type: DNA

A:Residues: 1-67 <JBI>

A:Cross-references: EMBL:M38723

R;James, P.; Hall, B.D.; Whelen, S.; Craig, E.A.

Gene 122, 101-110, 1992

A:Title: Multiple protein tyrosine phosphatase-encoding genes in the yeast Saccharomyces

A:Reference number: JC1484; MUID:93083970; PMID:1452018
A:Accession: JC1484
A:Molecule type: DNA
A:Residues: 1-370,'S',372-659,'GA',662-750 <JAW>
C:Genetics:
A:Gene: SGD,PTP2
A:Cross-references: SGD:S0005734; MIPS:YOR208w
A:Map position: 15R
C:Superfamily: protein-tyrosine-phosphatase homology
F:408-726/Domain: protein-tyrosine-phosphatase homology <PTP>
F:669-674/Region: nucleotide binding #status predicted
F:666/Active site: Cys (phosphocysteine intermediate) #status predicted
F:662/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.6%; Score 12; DB 2; Length 750;
Best Local Similarity 100.0%; Pred. No. 0.0026;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHC5AGCGRTGV 238
Db 664 VHC5AGCGRTGV 675

RESULT 2
S28392
A:Title: Schizosaccharomyces pombe
C:Keywords: Schizosaccharomyces pombe
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Dec-1999
C:Accession: S28392; T37537
R:Miller, J.B.A.; Lemaers, G.; Russell, P.
EMBO J. 11, 4933-4941, 1992
A:Title: Pyp3 PTPase acts as a mitotic inducer in fission yeast.
A:Reference number: S28392; MUID:93099868; PMID:1464318
A:Accession: S28392
A:Molecule type: DNA
A:Residues: 1-303 <ML>
A:Cross-references: EMBL:X69994; NID:G5017; PIDN:CAA49609.1; PID:G5018
R:Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, August 1997
A:Reference number: Z21721
A:Accession: T37537
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-303 <MR>
A:Cross-references: EMBL:Z98595; PIDN:CAB11188.1; GSPDB:GN00066; SPDB:SPAC11E3.09
A:Experimental source: strain 972h-; cosmid c11E3
C:Genetics:
A:Gene: pyp3
A:Map position: 1
A:Introns: 96/3
C:Superfamily: Schizosaccharomyces protein-tyrosine-phosphatase, nonreceptor type pyp3;
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:49-281/Domain: protein-tyrosine-phosphatase homology <PTP>
F:227/Active site: Cys (phosphocysteine intermediate) #status predicted
F:233/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.4%; Score 11; DB 1; Length 303;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHC5AGCGRTG 237
Db 225 VHC5AGCGRTG 235

RESULT 3
B44390
A:Title: Schizosaccharomyces pombe
C:Keywords: Schizosaccharomyces pombe
C:Date: 03-May-1994 #sequence_revision 26-May-1994 #text_change 11-Jun-1999
C:Accession: B44390; S71952; S27876

R:Matthews, R.J.; Bowne, D.B.; Flores, E.; Thomas, M.L.
Mol. Cell. Biol. 12, 2396-2405, 1992
A:Title: Characterization of hematopoietic intracellular protein tyrosine phosphatases: Csk, and threonine-rich sequences.
A:Reference number: A44390; MUID:92236615; PMID:1373816
A:Accession: B44390
A:Molecule type: mRNA
A:Residues: 1-802 <MF>
A:Cross-references: GB:M90388; NID:G200522; PIDN:AAA39994.1; PID:G200523
R:Cloutier, J.F.; Veillette, A.
EMBO J. 15, 4909-4918, 1996
A:Title: Association of inhibitory tyrosine protein kinase p50(csk) with protein tyrosine phosphatase p50(csk) with protein tyrosine phosphatase p50(csk)
A:Reference number: S71952; MUID:97045099; PMID:8890164
A:Accession: S71952
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 495-789 <CLO>
C:Comment: This protein is found primarily in hematopoietic tissues.
C:Genetics:
A:Gene: 702pep
C:Complex: Physically associates with inhibitory tyrosine protein kinase Csk; interaction
C:Function:
A:Description: probably an effector and/or regulator of tyrosine protein kinase csk in T-cells
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 8; protein-tyrosine-phosphatase, nonreceptor type 8; phosphoric monoester hydrolase; tyrosine-specific phosphatase
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:54-278/Domain: protein-tyrosine-phosphatase homology <PTP>
F:497-802/Region: glutamic acid/proline/serine/threonine-rich
F:613-621/Region: proline-rich
F:688-695/Region: proline-rich
F:227/Active site: Cys (phosphocysteine intermediate) #status predicted
F:233/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.4%; Score 11; DB 1; Length 802;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 228 HCSAGCGRTGV 238
Db 226 HCSAGCGRTGV 236

RESULT 4
A41109
A:Title: protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN3, nonreceptor type 3 [validated] - human
N:Alternate names: PTPN1
C:Species: Homo sapiens (man)
C:Date: 27-Mar-1992 #sequence_revision 02-May-1994 #text_change 21-Jun-2002
C:Accession: A41109; I55698
R:Yang, Q.; Tonks, N.K.
Proc. Natl. Acad. Sci. U.S.A. 88, 5949-5953, 1991
A:Title: Isolation of a cDNA clone encoding a human protein-tyrosine phosphatase with homology to the protein-tyrosine phosphatase family
A:Reference number: A41109; MUID:91296738; PMID:1648725
A:Accession: A41109
A:Molecule type: mRNA
A:Residues: 1-913 <YAN>
A:Cross-references: GB:M64572; NID:G179912; PIDN:AAA35647.1; PID:G179913
R:Ikuta, S.; Itoh, F.; Hinoda, Y.; Toyota, M.; Makiguchi, Y.; Inai, K.; Yachi, A.
J. Gastroenterol. 29, 727-732, 1994
A:Title: Expression of cytoskeletal-associated protein tyrosine phosphatase PTPN1 mRNA in human colon cancer cells
A:Reference number: I55698; MUID:95179278; PMID:7874267
A:Accession: I55698
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 899-913 <RES>
A:Cross-references: GB:S76309; NID:G913165; PIDN:AAB33583.1; PID:G913166
C:Genetics:
A:Gene: GDB:PTPN3
A:Cross-references: GDB:131386; OMIM:176877
A:Map position: 9c31-9q31
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; phosphatase
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
F:516-590/Domain: GLGF domain homology <GLG>

F;670-990/Domain: protein-tyrosine-phosphatase homology <PTP>
F;842/Active site: Cys (phosphocysteine intermediate) #status predicted
F;848/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.4%; Score 11; DB 1; Length 913;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 KNRYKDVLPYD 69
Db 673 KNRYKDVLPYD 683
|||||

RESULT 5
S50578
hypothetical protein YER075c - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 28-May-1993 #sequence_revision 24-Feb-1995 #text_change 23-Mar-2001
C;Accession: S50578
R;Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A;Description: The sequence of S. cerevisiae lambda clone 3612 and cosmid 9747.
A;Reference number: S50438
A;Accession: S50578
A;Molecule type: DNA
A;Residues: 1-928 <DIE>
A;Cross-references: EMBL:U18814; NID:g603309; PIDN:AAB64614.1; PID:g603312; MIPS:YER075c
C;Genetics:
A;Gene: SGD:PTP3
A;Cross-references: SGD:S0000877; MIPS:YER075c
A;Map position: 5R
C;Superfamily: protein-tyrosine-phosphatase homology
C;Keywords: phosphoprotein
F;527-867/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;804/Active site: Cys (phosphocysteine intermediate) #status predicted
F;810/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.4%; Score 11; DB 2; Length 928;
Best Local Similarity 100.0%; Pred. No. 0.031;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCSAGCGRTG 237
Db 802 VHCSAGCGRTG 812
|||||

RESULT 6
T49403
related to protein-tyrosine-phosphatase [imported] - Neurospora crassa
N;Alternate names: protein B1D4.180
C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
C;Accession: T49403
R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000
A;Reference number: 225022
A;Accession: T49403
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1132 <SCH>
A;Cross-references: EMBL:AL355928; GSPDB:GN00116; NCSP:B1D4.180
A;Experimental source: BAC clone B1D4; strain OR74A
C;Genetics:
A;Gene: NCSP:B1D4.180
A;Map position: 6
A;Introns: 670/3; 1104/2

Query Match 2.4%; Score 11; DB 2; Length 1132;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCSAGCGRTG 237
Db 802 VHCSAGCGRTG 812
|||||

Db 904 VHCSAGCGRTG 914

RESULT 7
JC4155
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - human
N;Alternate names: PEZ protein; protein-tyrosine-phosphatase/ezrin-like protein
C;Species: Homo sapiens (man)
C;Date: 27-Aug-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
C;Accession: JC4155
R;Smith, A.L.; Mitchell, P.J.; Shipley, J.; Gusterson, B.A.; Rogers, M.V.; Crompton, M.R. Biochem. Biophys. Res. Commun. 209, 959-965, 1995
A;Title: PEZ: a novel human cDNA encoding protein tyrosine phosphatase-and ezrin-like domain
A;Reference number: JC4155; MUID:95251727; PMID:7733990
A;Accession: JC4155
A;Molecule type: mRNA
A;Residues: 1-1187 <SMI>
A;Cross-references: EMBL:X82676; NID:g3929753; PIDN:CAA57993.1; PID:g805029
A;Experimental source: breast
C;Genetics:
A;Gene: GDB:PTPN14
A;Cross-references: GDB:454485
A;Map position: 1q32.2-1q32.2
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;23-302/Domain: protein 4.1 membrane-binding domain homology <B41>
F;566-575/Region: proline-rich
F;709-716/Region: acidic
F;933-1169/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1121/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1127/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.4%; Score 11; DB 1; Length 1187;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 YIATQGLPHT 111
Db 979 YIATQGLPHT 989
|||||

RESULT 8
JC2366
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 14 - mouse
N;Alternate names: PEZ protein; protein-tyrosine-phosphatase PTP36; protein-tyrosine-phos
C;Species: Mus musculus (house mouse)
C;Date: 24-Feb-1995 #sequence_revision 23-Feb-1996 #text_change 21-Jul-2000
C;Accession: JC2366
R;Sawada, M.; Ogata, M.; Fujino, Y.; Hamaoka, T. Biochem. Biophys. Res. Commun. 203, 479-484, 1994
A;Title: cDNA cloning of a novel protein tyrosine phosphatase with homology to cytoskeleton
A;Reference number: JC2366; MUID:94354845; PMID:8074693
A;Accession: JC2366
A;Molecule type: mRNA
A;Residues: 1-1189 <SAW>
A;Cross-references: GB:D31842; NID:g507330; PIDN:BAA06628.1; PID:g507331
A;Experimental source: thymus
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 14; protein 4.1 membrane-b
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F;23-302/Domain: protein 4.1 membrane-binding domain homology <B41>
F;566-575/Region: proline-rich
F;712-718/Region: acidic
F;935-1171/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;1123/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1129/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.4%; Score 11; DB 1; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 YIATQGLPHT 111
Db 981 YIATQGLPHT 991
|||||

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: C96741
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-340 <STO>
 A:Cross-references: GB:AE005173; NID:97239513; PIDN:AAF43239.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F14023.24
 A:Map position: 1
 C:Superfamily: Dictyostelium protein-tyrosine-phosphatase, nonreceptor type 2; protein-ty

Query Match 2.2%; Score 10; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 IATQGPLPHT 111
 |||||
 DB 135 IATQGPLPHT 144
 |||||

RESULT 12
 S48748
 protein-tyrosine-phosphatase (EC 3.1.3.48), probable nonreceptor type 12 splice form - r
 C:Species: *Rattus norvegicus* (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: S48748
 R:Moriyama, T.; Kawanishi, S.; Inoue, T.; Inai, E.; Kaneko, T.; Xia, C.; Takenaka, M.; No
 FEBS Lett. 353, 305-308, 1994
 A:Title: cDNA cloning of a cytosolic protein tyrosine phosphatase (RKPTP) from rat kidney
 A:Reference number: S48748; MUID:95046282; PMID:7957881
 A:Accession: S48748
 A:Molecule type: mRNA
 A:Residues: 1-382 <MOR>
 A:Cross-references: GB:D38072; NID:9567262; PIDN:BAA07266.1; PID:G699627
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosph
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:58-282/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:231/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:237/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.2%; Score 10; DB 1; Length 382;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 HCSAGCGRTG 237
 |||||
 DB 230 HCSAGCGRTG 239
 |||||

RESULT 13
 A57068
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)
 N:Alternate names: leukocyte antigen-related protein LAR
 C:Species: *Mus musculus* (house mouse)
 C:Date: 03-Oct-1995 #sequence_revision 09-Mar-1996 #text_change 23-Jul-1999
 C:Accession: A57068; S40280
 R:Schaaapveld, R.Q.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis, D.;
 Genomics 27, 124-130, 1995
 A:Title: The mouse gene *Lar* encoding the leukocyte common antigen-related molecule LAR.
 A:Reference number: A57068; MUID:95394448; PMID:7665159
 A:Accession: A57068
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-582 <SCH>
 A:Cross-references: GB:D37988; NID:993005; PIDN:CAA86070.1; PID:G993006
 R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
 submitted to the EMBL Data Library, June 1993
 A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
 A:Reference number: S40280

Query Match 2.2%; Score 10; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 IATQGPLPHT 111
 |||||
 DB 135 IATQGPLPHT 144
 |||||

RESULT 11
 C96741
 Hypothetical protein F14023.24 [imported] - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
 C:Accession: C96741
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: C96741
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-340 <STO>
 A:Cross-references: GB:AE005173; NID:97239513; PIDN:AAF43239.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F14023.24
 A:Map position: 1
 C:Superfamily: Dictyostelium protein-tyrosine-phosphatase, nonreceptor type 2; protein-ty

Query Match 2.2%; Score 10; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 IATQGPLPHT 111
 |||||
 DB 135 IATQGPLPHT 144
 |||||

RESULT 12
 S48748
 protein-tyrosine-phosphatase (EC 3.1.3.48), probable nonreceptor type 12 splice form - r
 C:Species: *Rattus norvegicus* (Norway rat)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
 C:Accession: S48748
 R:Moriyama, T.; Kawanishi, S.; Inoue, T.; Inai, E.; Kaneko, T.; Xia, C.; Takenaka, M.; No
 FEBS Lett. 353, 305-308, 1994
 A:Title: cDNA cloning of a cytosolic protein tyrosine phosphatase (RKPTP) from rat kidney
 A:Reference number: S48748; MUID:95046282; PMID:7957881
 A:Accession: S48748
 A:Molecule type: mRNA
 A:Residues: 1-382 <MOR>
 A:Cross-references: GB:D38072; NID:9567262; PIDN:BAA07266.1; PID:G699627
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12; protein-tyrosine-phosph
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:58-282/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:231/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:237/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.2%; Score 10; DB 1; Length 382;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 228 HCSAGCGRTG 237
 |||||
 DB 230 HCSAGCGRTG 239
 |||||

RESULT 13
 A57068
 protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type f - mouse (fragment)
 N:Alternate names: leukocyte antigen-related protein LAR
 C:Species: *Mus musculus* (house mouse)
 C:Date: 03-Oct-1995 #sequence_revision 09-Mar-1996 #text_change 23-Jul-1999
 C:Accession: A57068; S40280
 R:Schaaapveld, R.Q.J.; van den Maagdenberg, A.M.J.M.; Schepens, J.T.G.; Olde Weghuis, D.;
 Genomics 27, 124-130, 1995
 A:Title: The mouse gene *Lar* encoding the leukocyte common antigen-related molecule LAR.
 A:Reference number: A57068; MUID:95394448; PMID:7665159
 A:Accession: A57068
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-582 <SCH>
 A:Cross-references: GB:D37988; NID:993005; PIDN:CAA86070.1; PID:G993006
 R:Hendriks, W.; Brugman, C.; Zeeuwen, P.; Schepens, J.; Wieringa, B.
 submitted to the EMBL Data Library, June 1993
 A:Description: Assessment of the expression levels of murine protein-tyrosine phosphatase
 A:Reference number: S40280

A/Accession: S40280
 A/Molecule type: mRNA
 A/Residues: 116-221 <HEN>
 A/Cross-references: EMBL:Z23049; NID:g438135; PIDN:CAR80584.1; PID:g438136
 C/Genetics:
 A/Gene: Ptpfr
 C/Superfamily: leukocyte antigen-related protein; fibronectin type III repeat homology;
 C/Keywords: glycoprotein; phosphoprotein; phosphoric monoester hydrolase; transmembrane
 F;1-582/Domain: leukocyte common antigen cytosolic domain homology (fragment) <LAC>
 F;50-271/Domain: protein-tyrosine-phosphatase homology <PTP>
 F;339-562/Domain: protein-tyrosine-phosphatase homology <PTP2>
 F;223/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;229/Binding site: substrate phosphate (Arg) #status predicted
 F;514/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;520/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.2%; Score 10; DB 2; Length 582;
 Best Local Similarity 100.0%; Pred. No. 0.2; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0;

QY 100 AYIATQGGLP 109
 |||||
 Db 94 AYIATQGGLP 103

RESULT 14
 B53978
 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type PTPX10 - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 22-Jun-1999
 C/Accession: B53978
 R/Del Vecchio, R.L.; Tonks, N.K.
 J. Biol. Chem. 269, 19639-19645, 1994
 A/Title: Characterization of two structurally related Xenopus laevis protein tyrosine ph
 A/Reference number: A53978; MUID:94308257; PMID:8034733
 A/Accession: B53978
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-597
 A/Cross-references: GB:L33099; NID:g495671; PIDN:AAA21728.1; PID:g495672
 A/Experimental source: ovary
 A/Note: sequence extracted from NCBI backbone (NCBIN:149759, NCBIPI:149760)
 C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 9; cellular retinaldehyde-
 C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
 F;38-227/Domain: cellular retinaldehyde-binding protein homology <CRB>
 F;328-564/Domain: protein-tyrosine-phosphatase homology <PTP>
 F;516/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;522/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.2%; Score 10; DB 2; Length 597;
 Best Local Similarity 100.0%; Pred. No. 0.21; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0;

QY 100 AYIATQGGLP 109
 |||||
 Db 372 AYIATQGGLP 381

RESULT 15
 A53978
 protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type PTPX1 - African clawed frog
 C/Species: Xenopus laevis (African clawed frog)
 C/Date: 25-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 24-Apr-1998
 C/Accession: A53978
 R/Del Vecchio, R.L.; Tonks, N.K.
 J. Biol. Chem. 269, 19639-19645, 1994
 A/Title: Characterization of two structurally related Xenopus laevis protein tyrosine ph
 A/Reference number: A53978; MUID:94308257; PMID:8034733
 A/Accession: A53978
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-694

A/Experimental source: ovary
 A/Note: sequence extracted from NCBI backbone (NCBIN:149756, NCBIPI:149758)
 C/Superfamily: protein-tyrosine-phosphatase, nonreceptor type 9; cellular retinaldehyde-
 C/Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatas
 F;38-227/Domain: cellular retinaldehyde-binding protein homology <CRB>
 F;425-561/Domain: protein-tyrosine-phosphatase homology <PTP>
 F;613/Active site: Cys (phosphocysteine intermediate) #status predicted
 F;619/Binding site: substrate phosphate (Arg) #status predicted

Query Match 2.2%; Score 10; DB 2; Length 694;
 Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;
 Matches 10; Conservative 0;

QY 100 AYIATQGGLP 109
 |||||
 Db 469 AYIATQGGLP 478

Search completed: August 17, 2004, 20:53:05
 Job time : 24 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:44:41 ; Search time 14 Seconds
(without alignments)

1703.438 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 458

Sequence: 1 MSRLSARSFLERLARGG.....NLGRPKGRDPFPAEWTRV 458

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 141681 seqs, 52070155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	458	100.0	458	1 PTNI_HUMAN	Q99522 homo sapien
2	12	2.6	750	1 PTP2_YEAST	P29461 saccharomyc
3	11	2.4	303	1 PYP3_SCHPO	P2587 schizosacch
4	11	2.4	802	1 PTP8_MOUSE	P29352 mus musculu
5	11	2.4	807	1 PTN8_HUMAN	Q9Y2R2 homo sapien
6	11	2.4	913	1 PTN3_HUMAN	P26045 homo sapien
7	11	2.4	928	1 PTP3_YEAST	P40048 saccharomyc
8	11	2.4	1187	1 PTNE_HUMAN	Q15678 homo sapien
9	11	2.4	1189	1 PTNE_MOUSE	Q62130 mus musculu
10	10	2.2	775	1 PTNC_MOUSE	P35831 mus musculu
11	10	2.2	780	1 PTNC_HUMAN	Q05209 homo sapien
12	10	2.2	1001	1 PTPX_MOUSE	P80560 mus musculu
13	10	2.2	1004	1 PTPX_RAT	O63475 rattus norv
14	10	2.2	1013	1 PTPX_MACNE	O02895 macaca neme
15	10	2.2	1015	1 PTPF_HUMAN	Q92932 homo sapien
16	10	2.2	1897	1 PTPF_HUMAN	P10586 homo sapien
17	10	2.2	1948	1 PTNS_HUMAN	Q13332 homo sapien
18	9	2.0	979	1 PTEN_BOVIN	P56722 bos taurus
19	9	2.0	979	1 PTEN_HUMAN	Q16849 homo sapien
20	9	2.0	979	1 PTEN_MOUSE	Q60673 mus musculu
21	9	2.0	983	1 PTPN_RAT	Q63259 rattus norv
22	9	2.0	1216	1 PTPD_HUMAN	Q16827 homo sapien
23	9	2.0	1422	1 PTPG_CHICK	Q98936 gallus gall
24	9	2.0	1442	1 PTPG_MOUSE	Q05909 mus musculu
25	9	2.0	1445	1 PTPG_HUMAN	P23470 homo sapien
26	9	2.0	1912	1 PTPD_HUMAN	P23468 homo sapien
27	9	2.0	2200	1 LAR_CAEL	Q9bm88 caenorhabd
28	8	1.7	294	1 HDI_BRANA	P46606 brassica na
29	8	1.7	601	1 SG2_RANRI	P30945 rana ridibu
30	8	1.7	764	1 GLGE_ANASP	Q8YXK9 anabaena sp
31	8	1.7	1174	1 PTNL_HUMAN	Q16825 homo sapien
32	8	1.7	1175	1 PTNL_RAT	Q62728 rattus norv
33	8	1.7	1176	1 PTNL_MOUSE	Q62136 mus musculu

ALIGNMENTS

RESULT 1

ID	PTNI_HUMAN	STANDARD;	PRT;	458 AA.
AC	Q99522;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Protein-tyrosine phosphatase, non-receptor type 18 (EC 3.1.3.48)			
DE	(Brain-derived phosphatase).			
GN	PTPN18 OR BDPI.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]_SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND CHARACTERIZATION.			
RP	TISSUE=Brain;			
RC	MEDLINE=97108674; PubMed=8950995;			
RX	Kim Y.W., Wang H.Y., Sures I., Lammers R., Martell K.J., Ullrich A.;			
RA	"Characterization of the PEST family protein tyrosine phosphatase			
RT	BDPI."			
RL	OncoGene 13:2275-2279(1996).			
CC	FUNCTION: Differentially dephosphorylate autophosphorylated			
CC	tyrosine kinases which are known to be overexpressed in tumor			
CC	tissues.			
CC	CAATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein			
CC	tyrosine + phosphate.			
CC	TISSUE SPECIFICITY: Expressed in brain, colon and several tumor-			
CC	derived cell lines.			
CC	SIMILARITY: Belongs to the protein-tyrosine phosphatase family.			
CC	Non-receptor class subfamily.			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; X79568; CAA56105.1; ..			
DR	HSSP; Q06124; 2SHP.			
DR	Genew; HGNC:9649; PTPN18.			
DR	MIM; 606587; ..			
DR	GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. .; TAS.			
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.			
DR	InterPro; IPR000387; TYR phosphatase.			
DR	InterPro; IPR000242; TYR PP.			
DR	Pfam; PF00102; Y phosphatase; 1.			
DR	PRINTS; PRA00700; PRTYPHPTASE.			
DR	SMART; SM00194; PTPC; 1.			
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.			
DR	PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.			
DR	PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 1.			
KW	Hydrolase.			
DOMAIN	26 291			PROTEIN-TYROSINE PHOSPHATASE.

```

FT ACT_SITE 229 229 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY)
SQ SEQUENCE 458 AA; 50384 MW; 46BCA1E17C2C78B1 CRC64;

Query Match 100.0%; Score 458; DB 1; Length 458;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRLDSARGLRLERARGREGAVLAGESFDIQACSAWKAADGVSTVAGSPENVRKN 60
DB 1 MSRLDSARGLRLERARGREGAVLAGESFDIQACSAWKAADGVSTVAGSPENVRKN 60

QY 61 RYKDLVYDQTRVLSLQBEHSDYINGNFRIGVDGSLAYIATQGPLHTLLDFWRLVW 120
DB 61 RYKDLVYDQTRVLSLQBEHSDYINGNFRIGVDGSLAYIATQGPLHTLLDFWRLVW 120

QY 121 EFGVKVILMACREIENGKRCERYWAOEPLQTLGFCITLKEKWLNEIDIMLTLLKVT 180
DB 121 EFGVKVILMACREIENGKRCERYWAOEPLQTLGFCITLKEKWLNEIDIMLTLLKVT 180

QY 181 QKERSVYQLQYMSWPDGVPSSPDHMLAVVEARLQSGPEPLCVHCSAGCGRTGVLC 240
DB 181 QKERSVYQLQYMSWPDGVPSSPDHMLAVVEARLQSGPEPLCVHCSAGCGRTGVLC 240

QY 241 TVDVVRQLLTOMIPPFDSFLDVVVKMKRKPAAVQTEQRYFLYHTVAQMFCSLQNAS 300
DB 241 TVDVVRQLLTOMIPPFDSFLDVVVKMKRKPAAVQTEQRYFLYHTVAQMFCSLQNAS 300

QY 301 PHYQNIKENCAPLYDDALFRTQALAI PRPGGVLSRSVPGSGHAMADTYAEQKR 360
DB 301 PHYQNIKENCAPLYDDALFRTQALAI PRPGGVLSRSVPGSGHAMADTYAEQKR 360

QY 361 GAPAGAGSGTGTGTGARGSAEAPLYSKVT PRAQPGHAEDARGTLGPRVPADQSPAG 420
DB 361 GAPAGAGSGTGTGTGARGSAEAPLYSKVT PRAQPGHAEDARGTLGPRVPADQSPAG 420

QY 421 SGAYEDVAGGAQTGGLGNLRIGRPGKPRPPAEWTRV 458
DB 421 SGAYEDVAGGAQTGGLGNLRIGRPGKPRPPAEWTRV 458

RESULT 2
PTP2_YEAST STANDARD; PRT; 750 AA.
AC P29461;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase 2 (EC 3.1.3.48) (PTPase 2).
GN PTP2 OR YOR208W
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9220559; PubMed=1577774;
RA Guan K., Deschenes R.J., Dixon J.E.;
RT "Isolation and characterization of a second protein tyrosine
phosphatase gene, PTP2, from Saccharomyces cerevisiae.";
RL J. Biol. Chem. 267:10024-10030(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196117; PubMed=1549598;
RA Ota I.M., Varshavsky A.;
RT "A gene encoding a putative tyrosine phosphatase suppresses lethality
of an N-end rule-dependent mutant.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:2355-2359(1992).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92196117; PubMed=1549598;
RA James P., Hall B.D., Whelen S., Craig E.A.;
RL Submitted (JUL-1991) to the EMBL/GenBank/DBJ databases.
RN [4]

```

```

RP SEQUENCE FROM N.A.
RA Hughes B., Pohl T.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May be implicated in the ubiquitin-mediated protein
degradation pathway. May be involved in the regulation of MAP
kinase FUS3.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
CC
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CC
CC EMBL; M85287; -; NOT ANNOTATED_CDS.
DR EMBL; M82872; AAA34922.1; -.
DR EMBL; M38723; AAB59323.1; -.
DR EMBL; Z75116; CAA99423.1; -.
DR PIR; S67100; S67100.
DR HSSP; F18052; 11FO.
DR Germonline; 143796; -.
DR SGD; S0005734; PTP2.
DR GO; GO:0005634; C:nucleus; IDA.
DR InterPro; IPR00387; TYR_phosphatase.
DR InterPro; IPR00242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PK00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
FT ACT_SITE 666 666 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY)
FT CONFLICT 371 371 L -> S (IN REF. 3).
FT CONFLICT 474 475 KL -> NV (IN REF. 1).
FT CONFLICT 660 661 SP -> GA (IN REF. 3).
SQ SEQUENCE 750 AA; 85868 MW; 1033D2F0AA23BD35 CRC64;

Query Match 2.6%; Score 12; DB 1; Length 750;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VHCAGCGCGRTGV 238
DB 664 VHCAGCGCGRTGV 675

RESULT 3
PYP3_SCHPO STANDARD; PRT; 303 AA.
ID PYP3 SCHPO
AC P32587;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase 3 (EC 3.1.3.48) (PTPase 3).
GN PYP3 OR SPAC11E3.09.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9309868; PubMed=1464318;
RA Millar J.B.A., Lenaers G., Russell P.;
RT "Pyp3 PTPase acts as a mitotic inducer in fission yeast.";

```

RL ENBO J. 11:4933-4941(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sources J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Ganties S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney K., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Aert R., Robben J., Grymponrez B.,
 RA Waltiens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Halbert H.,
 RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Gageau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerutti L., Lowe T., McCombe W.R., Paulsen I., Pocashkin J.,
 RA Sipakowski G.V., Ussery D., Barrrell B.G., Nurse P.;
 RT The genome sequence of *Schizosaccharomyces pombe*.;
 RL Nature 415:871-880(2002).
 CC -1- FUNCTION: Contributes to dephosphorylation of tyrosine 15 of
 CC cdc2.
 CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC -1- Non-receptor class subfamily.
 CC -----
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 CC -----
 CC ENBL; X59994; CAA949609.1; -;
 CC ENBL; Z98595; CAB11188.1; -;
 CC PIR; S28392; S28392.
 CC HSP; P38827; IRPM.
 CC GeneDB Spombe; SPAC11E3.09; -;
 CC InterPro; IPR000387; TYR phosphatase.
 CC InterPro; IPR000242; Tyr_PP.
 CC Pfam; PF00102; Y_phosphatase; 1.
 CC PRINTS; PR00700; PTRYPHPTASE.
 CC SMART; SM00194; PTEC; 1.
 CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
 CC PROSITE; PS50055; TYR_PHOSPHATASE_PP; 1.
 CC Call division: Mitosis; Hydrolase.
 CC ACT_SITE 227 227 PHOSPHOCYCSTEINE INTERMEDIATE (BY
 CC SIMILARITY).
 CC SEQUENCE 303 AA; 34593 MW; 6ED642C918B32791 CRC64;
 SQ

```

RESULT 4
PTNM_MOUSE STANDARD; PRT; 802 AA.
AC P29352;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 8 (EC 3.1.3.48)
DE Hematopoietic cell protein-tyrosine phosphatase 702-PBP).
GN PTPN8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92236615; PubMed=1373816;
RA Matthews R.J., Bowne D.B., Flores E., Thomas M.L.;
RT "Characterization of hematopoietic intracellular protein tyrosine
RT phosphatases: description of a phosphatase containing an SH2 domain
RT and another enriched in proline-, glutamic acid-, serine-, and
RT threonine-rich sequences."
RL Mol. Cell. Biol. 12:2396-2405(1992).
CC -1- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: Spleen, thymus, lymph node and bone marrow.
CC -1- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -----
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CC -----
DR EMBL; M90386; AAA39994.1; -.
DR PIR; B44390; B44390.
DR PDB; 1JEG; 31-OCT-01.
DR MGD; MGI:107170; Ptpn8.
DR InterPro; IPR000387; Tyr_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; ERTFPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; 3D-structure.
FT DOMAIN 23 298
FT ACT_SITE 227 227
FT PROTEIN-TYROSINE PHOSPHATASE.
FT PROPHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
SQ SEQUENCE 802 AA; 89714 MW; 0F1B45339BD4613E CRC64;
Query Match 2.4%; Score 11; DB 1; Length 802;
Best Local Similarity 100.0%; Pred. No. 0.014;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 228 HCSAGCGRTGV 238
DB 226 HCSAGCGRTGV 236
=====
RESULT 5
PTNM_HUMAN STANDARD; PRT; 807 AA.
AC Q9YR22; Q95063; Q95064;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

```

DE Protein-tyrosine phosphatase, non-receptor type 22 (EC 3.1.3.48)
 DE (hematopoietic cell protein-tyrosine phosphatase 702-P2P) (Lymphoid
 DE phosphatase) (Lyp).
 GN PTPN22 OR PTPN8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.
 RX MEDLINE=9916899; PubMed=10086674;
 RA Cohen S., Dadi H., Shaoul E., Sharfe N., Roifman C.M.;
 RT "Cloning and characterization of a lymphoid-specific, inducible human
 RT protein tyrosine phosphatase, Lyp.";
 RL Blood 93:2013-2024(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Liu T., Zhang J., Fu G., Zhang Q., Ye M., Zhou J., Wu J., Shen Y.,
 RA Yu M., Chen S., Mao M., Chen Z.;
 RT "Human protein tyrosine phosphatase (702p2p) homolog.";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Seems to act on Cbl. May play a role in regulating the
 CC function of Cbl and its associated protein kinases.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1; Synonyms=LyP1;
 CC IsoId=O9Y2R2-1; Sequence=Displayed;
 CC Name=2; Synonyms=LyP2;
 CC IsoId=O9Y2R2-2; Sequence=VSP_005134;
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in lymphoid tissues
 CC and cells. Isoform 1 is expressed in thymocytes and both mature B
 CC and T cells.
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -----
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 CC -----
 CC EMBL; AF001846; AAC00904.1; -;
 CC EMBL; AF001847; AAC00905.1; -;
 CC EMBL; AF077031; AAC27764.1; -;
 CC HSSP; P29350; 1GWZ.
 CC Genew; HGNC:9652; PTPN22.
 CC MIM; 600716;
 CC InterPro; IPR000387; TYR_phosphatase.
 CC InterPro; IPR000242; Tyr_PP.
 CC Pfam; PF00102; Y_phosphatase; 1.
 CC PRINTS; PR00700; PTPPHPTASE.
 CC SMART; SM00194; PTPC; 1.
 CC PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
 CC PROSITE; PSS0056; TYR_PHOSPHATASE 2; 1.
 CC PROSITE; PSS0055; TYR_PHOSPHATASE_PTP; 1.
 CC KX Hydrolase; Alternative splicing.
 CC DOMAIN 23 288
 CC ACT_SITE 227 287
 CC PROTEIN-TYROSINE PHOSPHATASE.
 CC PHOSPHOCYSTEINE INTERMEDIATE (BY
 CC SIMILARITY).
 CC ELHDDRSSPPPELPTLESEFFLEDCMOAQSIETVTSY
 CC PTFMNTSSKQKLTGKSKFTSKILRNKKKICNSC
 CC PPKPABSVSNSSFLNPGFANRSKPGKPRPPPTWNI
 CC -> GKNFSWL (In isoform 2).
 CC /FTid=VSP_005134.
 CC KP -> NA (IN REF. 1).
 CC V -> G (IN REF. 2).
 CC G -> V (IN REF. 2).
 CC I -> IV (IN REF. 1).
 CC CONFLICT 51 52
 CC CONFLICT 126 126
 CC CONFLICT 147 147
 CC CONFLICT 240 240

FT CONFLICT 420 420 L -> P (IN REF. 2).
 FT CONFLICT 620 620 R -> W (IN REF. 2).
 FT CONFLICT 742 742 P -> S (IN REF. 2).
 SQ SEQUENCE 807 AA; 91704 MW; 1ABE8AE89C9D9PBF CRC64;
 Query Match 2.4%; Score 11; DB 1; Length 807;
 Best Local Similarity 100.0%; Pred. No. 0.014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 228 HCSAGCGRTGV 238
 Db 226 HCSAGCGRTGV 236
 RESULT 6
 PTPN3 HUMAN
 ID PTPN3 HUMAN STANDARD; PRT; 913 AA.
 AC P26045.
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein tyrosine phosphatase, non-receptor type 3 (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase H1) (PTP-H1).
 DE PTPN3 OR PTPH1.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91296738; PubMed=1648725;
 RA Yang Q., Tonks N.K.;
 RT "Isolation of a cDNA clone encoding a human protein-tyrosine
 RT phosphatase with homology to the cytoskeletal-associated proteins
 RT band 4.1, ezrin, and talin.";
 RT Proc. Natl. Acad. Sci. U.S.A. 88:5949-5953(1991).
 RN [2]
 RP SEQUENCE OF 194-896 FROM N.A.
 RC TISSUE=Colon;
 RX MEDLINE=92327504; PubMed=1626183;
 RA Arimura Y., Hinoda Y., Itoh F., Takekawa M., Tsujisaki M., Adachi M.,
 RA Imai K., Yachi A.;
 RT "cDNA cloning of new protein tyrosine phosphatases in the human
 RT colon.";
 RT Tumour Biol. 13:180-186(1992).
 RN [3]
 RP SEQUENCE OF 899-913 FROM N.A.
 RX MEDLINE=95179278; PubMed=7874267;
 RA Ikuta S., Itoh F., Hinoda Y., Toyota M., Makiguchi Y., Imai K.,
 RA Yachi A.;
 RT "Expression of cytoskeletal-associated protein tyrosine phosphatase
 RT PTPH1 mRNA in human hepatocellular carcinoma.";
 RL J. Gastroenterol. 29:727-732(1994).
 CC -!- FUNCTION: May act at junctions between the membrane and the
 CC cytoskeleton.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -!- SIMILARITY: Contains 1 FERM domain.
 CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
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 CC -----
 CC EMBL; M64572; AAA35647.1; -;
 CC EMBL; S39392; AAB22439.2; -;

```

DR EMBL; S76309; AAB33583.1; -.
DR PIR; A41109; A41109.
DR HSP; P18031; LFTY.
DR Genew; HGNC:9655; PTPN3.
DR MIM; 176877; -.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; TAS.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
DR InterPro; IPR000298; Band 4.1.
DR InterPro; IPR001478; PDZ.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00373; Band 41; 1.
DR Pfam; PF00595; PDZ_1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00335; BAND41.
DR PRINTS; PR00700; PTPYHPHTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00228; PDZ; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM_1; 1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS50057; FERM_3; 1.
DR PROSITE; PS50106; PDZ; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
DR Structural protein; Cytoskeleton; Hydrolase.
KW DOMAIN 29 312 FERM.
FT DOMAIN 510 582 PDZ.
FT DOMAIN 670 913 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 842 842 PHOSPHOCYSTEINE INTERMEDIATE
FT ACT_SITE 842 842 (BY SIMILARITY).
SQ SEQUENCE 913 AA; 104029 MW; 29A539ACDE2F1515 CRC64;

Query Match 2.4%; Score 11; DB 1; Length 913;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 KRYKDVLPYD 69
DB 673 KRYKDVLPYD 683

RESULT 7
PTP3 YEAST
ID PTP3 YEAST STANDARD; PRT; 928 AA.
AC P40048;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase 3 (EC 3.1.3.48) (PTPase 3).
GN PTP3 OR YER075C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OC NCBI_TaxID=4932;
CX [1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RP MEDLINE=97367951; PubMed=9224718;
RX Zhan X.-L., Deschenes R.J., Guan K.-L.;
RT "Differential regulation of FUS3 MAP kinase by tyrosine-specific
RT phosphatases PTP2/PTP3 and dual-specificity phosphatase MS05 in
RT Saccharomyces cerevisiae.";
RL Genes Dev. 11:1690-1702(1997).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=S288C / AB972;
RX MEDLINE=97313264; PubMed=9169868;
RA Dietrich F.S., Mulligan J.T., Hennessy K.M., Yelton M.A., Allen E.,
RA Araujo R., Aviles E., Berio A., Brennan T., Carpenter J., Chen E.,
RA Cherry J.M., Chung E., Duncan M., Guzman E., Hartzell G.,
RA Hunnicke-Smith S., Hyman R.W., Kayser A., Komp C., Lashkari D., Lew H.,
RA Lin D., Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P.,

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RA Oh C., Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T.,
RA Smith V., Taylor P., Wei Y., Botstein D., Davis R.W.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome V.";
RL Nature 387:78-81(1997).
CC -!- FUNCTION: Major phosphatase responsible for tyrosine
CC dephosphorylation of MAP kinase FUS3 to inactivate its activity;
CC it also has important roles, along with MS05, in the inactivation
CC of FUS3 following pheromone stimulation.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -!- SIMILARITY: Contains 1 rhodanese domain.
CC
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CC
CC EMBL; AF06304; AAB70811.1; -.
CC EMBL; U18814; AAB64614.1; -.
CC PIR; S50578; S50578.
CC HSP; P29350; 1GMZ.
CC GerMOnline; 139155; -.
CC SGD; S000877; PTP3.
CC GO; GO:0005737; Cytoplasm; IDA.
CC GO; GO:0004725; F:protein tyrosine phosphatase activity; IDA.
CC GO; GO:0000173; P:inactivation of MAPK (osmolarity sensing); IMP.
CC GO; GO:0006470; P:protein amino acid dephosphorylation; IDA.
CC GO; GO:0000750; P:signal transduction during conjugation with. .; IMP.
CC InterPro; IPR001763; Rhodanese-like.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; TYR_PP.
CC Pfam; PF00581; Rhodanese; 1.
CC Pfam; PF01102; Y_phosphatase; 1.
CC PRINTS; PR00700; PTPYHPHTASE.
CC SMART; SM00194; PTPC; 1.
CC SMART; SM00450; RHOD; 1.
CC PROSITE; PS50206; RHODANESE_3; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
CC PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
FT DOMAIN 111 232 RHODANESE.
FT ACT_SITE 804 804 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT ACT_SITE 804 804 SIMILARITY).
FT DOMAIN 308 311 POLY-SER.
FT DOMAIN 592 597 POLY-THR.
FT DOMAIN 702 715 POLY-ASN.
FT DOMAIN 724 732 POLY-ASP.
SQ SEQUENCE 928 AA; 105250 MW; 6DEC5BA26B7ACBCB CRC64;

Query Match 2.4%; Score 11; DB 1; Length 928;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 227 VHC5AGCGRTG 237
DB 802 VHC5AGCGRTG 812

RESULT 8
PTNE HUMAN
ID PTNE HUMAN STANDARD; PRT; 1187 AA.
AC Q15678;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase pez).

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GN PTPN14 OR PEZ.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast carcinoma;
RX MEDLINE=95251727; PubMed=7733990;
RA Smith A.L., Mitchell P.J., Shipley J., Gusterson B.A., Rogers M.V.,
RA Crompton M.R.;
RT "Pez: a novel human cDNA encoding protein tyrosine phosphatase- and
RT ezrin-like domains";
RL Biochem Biophys Res Commun. 209:959-965(1995).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- TISSUE SPECIFICITY: Expressed in a variety of human tissues
CC including kidney, skeletal muscle, lung and placenta.
CC -!- SIMILARITY: Contains 1 FERM domain.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC
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CC
CC EMBL; X82676; CAA57993.1; -.
CC PIR; JC4155; JC4155.
CC HSSP; P29350; 1GWZ.
CC Genew; HGNC:9647; PTPN14.
CC MIN; 603155; -.
CC GO; GO:0004725; P:protein tyrosine phosphatase activity; TAS.
CC GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC InterPro; IPR000299; Band 4.1.
CC InterPro; IPR000387; TYR_Phosphatase.
CC InterPro; IPR000242; Tyr_Pp.
CC Pfam; PF00373; Band_41; 1.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00935; BAND41.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00295; B41; 1.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00660; FERM_1; 1.
CC PROSITE; PS00661; FERM_2; 1.
CC PROSITE; PS50057; FERM_3; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
CC structural protein; Cytoskeleton; Hydrolase.
FT DOMAIN 21 306 FERM.
FT ACT_SITE 1121 1121 (BY SIMILARITY).
FT DOMAIN 566 573 POLY-PRO.
FT DOMAIN 709 716 POLY-GLU.
SQ SEQUENCE 1187 AA; 135239 MW; 015760875E3574E3 CRC64;
Query Match 2.4%; Score 11; DB 1; Length 1187;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 YIATQGPLPHT 111
Db 979 YIATQGPLPHT 989

RESULT 9
PTNE MOUSE
ID PTNE_MOUSE STANDARD; PRT; 1189 AA.

AC O62130;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 14 (SC 3.1.3.48)
DE (Protein-tyrosine phosphatase PTP36).
GN PTPN14.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CB-17-SCID; TISSUE=Thymus;
RX MEDLINE=94354845; PubMed=8074693;
RA Sawada M., Ogata M., Fujino Y., Hamaoka T.;
RT "cDNA cloning of a novel protein tyrosine phosphatase with homology
RT to cytoskeletal protein 4.1 and its expression in T-lineage cells";
RL Biochem Biophys Res Commun. 203:479-484(1994).
CC -!- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF T CELL DEVELOPMENT.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- TISSUE SPECIFICITY: Thymus; in cells of both hematopoietic and
CC non-hematopoietic origins.
CC -!- SIMILARITY: Contains 1 FERM domain.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC
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CC
CC EMBL; D31842; BAA06628.1; -.
CC PIR; JC2366; JC2366.
CC HSSP; Q06124; 2SHP.
CC MGD; MGI:102467; Ptpn14.
CC InterPro; IPR000299; Band 4.1.
CC InterPro; IPR000387; TYR_Phosphatase.
CC InterPro; IPR000242; Tyr_Pp.
CC Pfam; PF00373; Band_41; 1.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00935; BAND41.
CC PRINTS; PR00700; PRTYPHPTASE.
CC SMART; SM00295; B41; 1.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00660; FERM_1; 1.
CC PROSITE; PS00661; FERM_2; 1.
CC PROSITE; PS50057; FERM_3; 1.
CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
CC structural protein; Cytoskeleton; Hydrolase.
FT DOMAIN 21 306 FERM.
FT ACT_SITE 1123 1123 (BY SIMILARITY).
FT DOMAIN 566 573 POLY-PRO.
FT DOMAIN 635 639 POLY-GLY.
FT DOMAIN 712 718 POLY-GLU.
SQ SEQUENCE 1189 AA; 135030 MW; 2B85B8EF9C723303 CRC64;
Query Match 2.4%; Score 11; DB 1; Length 1189;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 YIATQGPLPHT 111
Db 981 YIATQGPLPHT 991

RESULT 10
 PTNC_MOUSE
 ID PTNC_MOUSE STANDARD; PRT; 775 AA.
 AC P35831;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 12 (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase P19) (P19-PTP) (MPTP-PEST).
 GN PTPN12.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=9227214; PubMed=1590786;
 RX den Hertog J., Pals C.E., Jonk L.J., Kruijer W.;
 RA "Differential expression of a novel murine non-receptor protein
 RT tyrosine phosphatase during differentiation of P19 embryonal
 RT carcinoma cells.";
 RL Biochem. Biophys. Res. Commun. 184:1241-1249(1992).
 RN [2]
 RN REVISIONS TO 297-416.
 RP MEDLINE=93112015; PubMed=1472029;
 RX Takekawa M., Itoh F., Hinoda Y., Arimura Y., Toyota M., Sekiya M.,
 RA Adachi M., Imai K., Yachi A.;
 RA "Cloning and characterization of a human cDNA encoding a novel
 RT putative cytoplasmic protein-tyrosine-phosphatase.";
 RL Biochem. Biophys. Res. Commun. 189:1223-1230(1992).
 RN [3]
 RN SEQUENCE FROM N.A.
 RP STRAIN=BALB/c;
 RX MEDLINE=95289971; PubMed=7772023;
 RA Charest A., Wegner J., Shen S.H., Tremblay M.L.;
 RT "Murine protein tyrosine phosphatase-PEST, a stable cytosolic protein
 RT tyrosine phosphatase.";
 RL Biochem. J. 308:425-432(1995).
 CC -/- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -/- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -/- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.

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 CC EMBL; X63440; CAA45037.1; ALT_SEQ.
 CC EMBL; X86781; CAA60477.1; --
 CC PIR; S53345; S53345.
 CC HSSP; Q06124; 2SHP.
 CC DR MGD; MGI:104673; Ptpn12.
 CC InterPro; IPR000387; TYR_phosphatase.
 CC InterPro; IPR000242; Tyr_PP.
 CC Pfam; PF00102; Y_phosphatase; 1.
 CC PRINTS; PR00700; PRTYPHPTASE.
 CC SMART; SMO0194; PTPC; 1.
 CC PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
 CC Hydrolase.
 CC FT DOMAIN 27 291 PROTEIN-TYROSINE PHOSPHATASE.
 CC FT ACT_SITE 231 231 PHOSPHOCYSTEINE INTERMEDIATE (BY
 CC SIMILARITY).
 CC FT CONFLICT 296 296 K -> N (IN REF. 1).
 CC FT CONFLICT 328 328 KDSP -> DETS (IN REF. 1).
 CC FT CONFLICT 380 380 W -> V (IN REF. 1).
 CC FT

DR GO: GO:0005623; C:soluble fraction; TAS.
 DR GO: GO:0004726; F:non-membrane spanning protein tyrosine phosphatase; TAS.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; TAS.
 DR InterPro: IPR000387; Tyr phosphatase.
 DR InterPro: IPR000242; Tyr_PP.
 DR Pfam: PF00102; Y_phosphatase; 1.
 DR PRINTS: SM00194; PTPC; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
 DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolase; Disease mutation.
 FT DOMAIN 27 291
 FT ACT_SITE 231 291
 FT VARIANTS 61 61
 FT VARIANT K -> R (in colon cancer).
 FT CONFLICT 121 121 /FTID=VAR_006385.
 FT CONFLICT 322 322 V -> I (IN REF. 2).
 FT CONFLICT 322 322 V -> I (IN REF. 2).
 SQ SEQUENCE 780 AA; 88092 MW; 48FVE5FDAEF7512 CRC64;
 Query Match 2.2%; Score 10; DB 1; Length 780;
 Best Local Similarity 100.0%; Pred. No. 0.13;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 228 HCSAGCGRTG 237
 DB 230 HCSAGCGRTG 239
 RESULT 12
 ID_PTPX_MOUSE STANDARD; PRT; 1001 AA.
 AC P80560; 009134; F70328;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Receptor-type protein-tyrosine phosphatase N2 precursor (EC 3.1.3.48)
 DE (R-PTP-N2) (PTP IA-2beta) (Protein tyrosine phosphatase-NP) (PTP-NP).
 GN PTPRN2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR; TISSUE=Brain;
 RX MEDLINE=96281667; PubMed=8681804;
 RA Chiang M.-K., Flanagan J.G.;
 RT "PTP-NP, a new member of the receptor protein tyrosine phosphatase family, implicated in development of nervous system and pancreatic endocrine cells."
 RT Development 122:2239-2250(1996).
 RL [2]
 RN SEQUENCE OF 282-1001 FROM N.A.
 RP TISSUE=Neonatal brain;
 RC MEDLINE=96197307; PubMed=8637868;
 RX Lu J., Li Q., Xie H., Chen Z.-J., Borovitskaya A.E., Maclaren N.K.,
 RA Notkins A.L., Lan M.S.;
 RT "Identification of a second transmembrane protein tyrosine phosphatase, IA-2beta, as an autoantigen in insulin-dependent diabetes mellitus: precursor of the 37-kDa tryptic fragment."
 RT Proc. Natl. Acad. Sci. U.S.A. 93:2307-2311(1996).
 CC -!- FUNCTION: Implicated in development of nervous system and pancreatic endocrine cells.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1; Synonyms=type 1-PTP-NP;
 CC IsoId=P80560-1; Sequence=Displayed;
 CC Name=2; Synonyms=type 2-PTP-NP;
 CC IsoId=P80560-2; Sequence=Not described;
 CC -!- TISSUE SPECIFICITY: Pancreas and brain.
 CC -!- DEVELOPMENTAL STAGE: Expressed in early stages of pancreatic development. First expressed in day 8.5 embryos (E8.5) in the dorsal part of the midgut endoderm and by E9.5, in the pancreatic rudiment specifically in early endocrine progenitor cells. At later stages expressed in insulin- or glucagon-producing cells. During neural development, the type 2 PTP-NP is expressed in early stages of neurogenesis, and the type 1 weakly in the later stages.
 CC -!- PTM: Appears to undergo multiple proteolytic cleavage at consecutive basic residues (by similarity).
 CC -!- DISEASE: Autoantigen in insulin-dependent diabetes mellitus (IDDM).
 CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
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 CC EMBL: U57345; AAB06945.1; -;
 CC EMBL: U82439; AAB39996.1; -;
 CC HSSP: F18052; LYFO.
 CC MGD: MGI:107418; Ptpn2.
 CC InterPro: IPR000387; TYR_phosphatase.
 CC InterPro: IPR000242; Tyr_PP.
 CC Pfam: PF00102; Y_phosphatase; 1.
 CC PRINTS: PR0700; PTPPHPTASE.
 CC SMART: SM00194; PTPC; 1.
 CC PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
 CC PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
 CC PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
 KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
 KW Diabetes mellitus; Alternative splicing.
 FT SIGNAL 1 27
 FT CHAIN 28 1001 RECEPTOR-TYPE PROTEIN-TYROSINE PHOSPHATASE N2. (POTENTIAL).
 FT DOMAIN 28 600 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 601 621 POTENTIAL.
 FT DOMAIN 622 1001 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 756 990 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 931 931 PHOSPHOCYSTEINE INTERMEDIATE (POTENTIAL).
 FT SITE 413 414 CLEAVAGE SITE (BY SIMILARITY).
 FT CARBOHYD 550 550 N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 370 371 MISSING (IN REF. 2).
 FT CONFLICT 395 395 H -> P (IN REF. 2).
 FT CONFLICT 411 411 I -> M (IN REF. 2).
 FT CONFLICT 414 414 S -> L (IN REF. 2).
 FT CONFLICT 586 586 L -> H (IN REF. 2).
 SQ SEQUENCE 1001 AA; 111554 MW; 6B73EACAS35D2BE5 CRC64;
 Query Match 2.2%; Score 10; DB 1; Length 1001;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 100 AVIATQGPLP 109
 DB 801 AVIATQGPLP 810
 RESULT 13
 ID_PTPX_RAT STANDARD; PRT; 1004 AA.
 AC Q63475.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Receptor-type protein-tyrosine phosphatase N2 precursor (EC 3.1.3.48)
 DE (R-PTP-N2) (PTP NE-6) (PTPNE6) (Phogrin).
 CC

GN PTPRN2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=New England Deaconess Hospital; TISSUE=Insulinoma;
RA Wasmeyer C., Hutton J.C.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Fitzgerald L.R., Walton K.M., Dixon J.E., Largent B.L.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Implicated in development of nervous system and
CC pancreatic endocrine cells.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Pancreas.
CC -!- PTM: Appears to undergo multiple proteolytic cleavage at
CC consecutive basic residues (By similarity).
CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Z50735; CAA90800.1; -.
CC DR EMBL; U73458; AAC08036.1; -.
CC DR HSSP; P18052; 1YFO.
CC DR InterPro; IPR000387; TYR_phosphatase.
CC DR InterPro; IPR000242; Tyr_PP.
CC DR Pfam; PF00102; Y_phosphatase; 1.
CC DR PRINTS; PR00700; PRTYPHPTASE.
CC DR SMART; SM00194; PTPC; 1.
CC DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
CC DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
CC KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane.
CC FT SIGNAL 1 27
CC FT CHAIN 28 1004
CC FT RECEPTOR-TYPE PROTEIN-TYROSINE
CC FT PHOSPHATASE N2.
CC FT EXTRACELLULAR (POTENTIAL).
CC FT POTENTIAL.
CC FT CYTOPLASMIC (POTENTIAL).
CC FT PROTEIN-TYROSINE PHOSPHATASE.
CC FT PHOSPHOCYSTEINE INTERMEDIATE (POTENTIAL).
CC FT ACT_SITE 934 934
CC FT CLEAVAGE_SITE (BY SIMILARITY).
CC FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 553 553
CC FT SEQUENCE 1004 AA; 111863 MW; A73929E11B486FB2 CRC64;
SQ
Query Match 2.2%; Score 10; DB 1; Length 1004;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 100 AYIATQGLPLP 109
DB 804 AYIATQGLPLP 813
RESULT 14
PTPX_MACNE
ID_PTPX_MACNE STANDARD; PRT; 1013 AA.
AC O02635;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Receptor-type protein-tyrosine phosphatase N2 precursor (EC 3.1.3.48)
DE PTPRN2.
GN Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreatic islets;
RX MEDLINE=97254813; PubMed=9100223;
RA Lagasse P., Jelinek L., Sexson S., Lofton-Day C.E., Breininger J.,
RA Sheppard J., Kindesvogel W., Hagopian W.A.;
RT "An islet-cell protein tyrosine phosphatase is a likely precursor to
RT the 37-kDa autoantigen in type 1 diabetes: human and macaque
RT sequences, tissue distribution, unique and shared epitopes, and
RT predictive autoantibodies.";
RL Mol. Med. 3:163-173(1997).
CC -!- FUNCTION: Implicated in development of nervous system and
CC pancreatic endocrine cells.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Brain, prostate, pancreatic islets. Lower
CC expression in spinal cord, thyroid, adrenal medulla and
CC gastrointestinal tract.
CC -!- PTM: Appears to undergo multiple proteolytic cleavage at
CC consecutive basic residues (By similarity).
CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U91574; AAC51186.1; -.
CC DR HSSP; P18052; 1YFO.
CC DR InterPro; IPR000387; TYR_phosphatase.
CC DR InterPro; IPR000242; Tyr_PP.
CC DR Pfam; PF00102; Y_phosphatase; 1.
CC DR PRINTS; PR00700; PRTYPHPTASE.
CC DR SMART; SM00194; PTPC; 1.
CC DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
CC DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
CC DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
CC KW Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane.
CC FT SIGNAL 1 19
CC FT CHAIN 20 1013
CC FT RECEPTOR-TYPE PROTEIN-TYROSINE
CC FT PHOSPHATASE N2.
CC FT EXTRACELLULAR (POTENTIAL).
CC FT POTENTIAL.
CC FT CYTOPLASMIC (POTENTIAL).
CC FT PROTEIN-TYROSINE PHOSPHATASE.
CC FT PHOSPHOCYSTEINE INTERMEDIATE (POTENTIAL).
CC FT CLEAVAGE_SITE (BY SIMILARITY).
CC FT N-LINKED (GLCNAC. . .) (POTENTIAL).
CC FT CARBOHYD 562 562
CC FT SEQUENCE 1013 AA; 111190 MW; 4808D43937A2EF59 CRC64;
SQ
Query Match 2.2%; Score 10; DB 1; Length 1013;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 100 AYIATQGLPLP 109
DB 813 AYIATQGLPLP 822
RESULT 15
PTPX_HUMAN

ID PTFX_HUMAN STANDARD; PRT; 1015 AA.
 AC Q92932; Q8N415; Q92662;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Receptor-type protein-tyrosine phosphatase N2 precursor (EC 3.1.3.48)
 DE (R-PTP-N2) (Islet cell autoantigen related protein) (ICAP) (IAR)
 DE (Phogrin).
 DE (Phogrin).
 GN PTPN22.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Pancreas;
 RX MEDLINE=97032784; PubMed=8878534;
 RA Kawasaki E., Hutton J.C., Eisenbarth G.S.;
 RT "Molecular cloning and characterization of the human transmembrane
 RT protein tyrosine phosphatase homologue, phogrin, an autoantigen of
 RT type 1 diabetes.";
 RL Biochem. Biophys. Res. Commun. 227:440-447(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Fetal brain;
 RX MEDLINE=97127415; PubMed=8954911;
 RA Smith P.D., Barker K.T., Wang J., Lu Y.-J., Shipley J., Crompton M.R.;
 RT "ICAPAR, a novel member of a new family of transmembrane, tyrosine
 RT phosphatase-like proteins.";
 RL Biochem. Biophys. Res. Commun. 229:402-411(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain and Pancreas;
 RX MEDLINE=96394649; PubMed=8798755;
 RA Cui L., Xu W.-P., de Alzpurua H.J., Schmidl R.S., Pallen C.J.;
 RT "Cloning and characterization of islet cell antigen-related protein-
 RT tyrosine phosphatase (PTP), a novel receptor-like PTP and autoantigen
 RT in insulin-dependent diabetes.";
 RL J. Biol. Chem. 271:24817-24823(1996).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Narusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Implicated in development of nervous system and
 CC pancreatic endocrine cells.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q92932-1; Sequence=displayed;
 CC Name=2;

CC IsoId=Q92932-2; Sequence=VSP_007779;
 CC Note=No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Highest levels in brain and pancreas. Lower
 CC levels in trachea, prostate, stomach and spinal chord.
 CC -!- DOMAIN: The cytoplasmic domain appears to contain the
 CC autoantigenic epitopes.
 CC -!- PTM: Appears to undergo multiple proteolytic cleavage at
 CC consecutive basic residues.
 CC -!- DISEASE: Autoantigen in insulin-dependent diabetes mellitus
 CC (IDDM).
 CC -!- MISCELLANEOUS: Optimum activity is measured at pH 4.5.
 CC -!- SIMILARITY: Contains 1 protein-tyrosine phosphatase domain.
 CC -----
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 CC -----
 CC EMBL; U66702; AAC50742.1; -;
 CC EMBL; Y08569; CAA69880.1; -;
 CC EMBL; AF007555; AAB63600.1; -;
 CC EMBL; BC034040; AAH34040.1; -;
 CC PIR; JC5062; JC5062.
 CC PIR; JC5263; JC5263.
 CC HSP; P18052; LYFO.
 CC Genew; HGNC:9677; PTPN22.
 CC MIM; 601698; -;
 CC GO; GO:0005887; C: integral to plasma membrane; TAS.
 CC GO; GO:0005001; P: transmembrane receptor protein tyrosine pho. .; TAS.
 CC GO; GO:0006470; P: protein amino acid dephosphorylation; TAS.
 CC InterPro; IPR003595; PTPC motif.
 CC InterPro; IPR000387; TYR_PTPase.
 CC InterPro; IPR000242; Tyr_PP.
 CC Pfam; PF00102; Y_PTPase.
 CC PRINTS; PR00700; PTPHPPTASE.
 CC SMART; SM00194; PTPC; 1.
 CC SMART; SM00404; PTPC motif; 1.
 CC PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
 CC PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
 CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
 CC Hydrolase; Receptor; Glycoprotein; Signal; Transmembrane;
 CC Diabetes mellitus; Alternative splicing.
 CC SIGNAL 1 21
 CC CHAIN 22 1015
 CC RECEPTOR-TYPE PROTEIN-TYROSINE
 CC PHOSPHATASE N2.
 CC EXTRACELLULAR (POTENTIAL).
 CC POTENTIAL.
 CC CYTOPLASMIC (POTENTIAL).
 CC PROTEIN-TYROSINE PHOSPHATASE.
 CC PHOSPHOCYSTEINE INTERMEDIATE (BY
 CC SIMILARITY).
 CC CLEAVAGE SITE (POTENTIAL).
 CC N-LINKED (GLCNAC. .) (POTENTIAL).
 CC Missing (in isoform 2).
 CC /FtId=VSP_007779.
 CC C->S: LOSS OF ACTIVITY.
 CC P -> S (IN REF. 2 AND 3).
 CC S -> G (IN REF. 2).
 CC S -> R (IN REF. 2).
 CC S -> N (IN REF. 2).
 CC S -> N (IN REF. 2).
 CC SEQUENCE 1015 AA; 111281 MW; 82AC3C9F59A6C97 CRC64;
 SQ
 Query Match 2.2%; Score 10; DB 1; Length 1015;
 Best Local Similarity 100.0%; Pred. No. 0.17;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 100 AYIATQGLP 109
 DB 815 AYIATQGLP 824

Search completed: August 17, 2004, 20:50:34
Job time : 20 secs

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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:48:22 ; Search time 44 Seconds
(without alignments)

3284.258 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 458
Sequence: 1 MSRLSDARSFLERLEARGG.....NLIRGPKGRDPPAEWTRV 458

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1017041 seqs, 315518202 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

1: SPTREMBL 25:*

2: sp_archea:*

3: sp_bacteria:*

4: sp_fungi:*

5: sp_human:*

6: sp_invertebrate:*

7: sp_mammal:*

8: sp_mhc:*

9: sp_organelle:*

10: sp_phage:*

11: sp_plant:*

12: sp_rodent:*

13: sp_virus:*

14: sp_vertebrate:*

15: sp_unclassified:*

16: sp_rvirus:*

17: sp_bacteriap:*

18: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	217	47.4	351	4 Q7Z637	Q7Z637 homo sapien
2	217	47.4	372	4 Q8TA96	Q8TA96 hmo sapien
3	32	7.0	453	11 Q922E3	Q922E3 mus musculus
4	32	7.0	453	11 Q61152	Q61152 mus musculus
5	29	6.3	453	11 P70602	P70602 rattus norv
6	12	2.6	258	13 Q90Y62	Q90Y62 brachydanio
7	12	2.6	487	5 Q9NL13	Q9NL13 brachyosteo
8	11	2.4	84	4 Q93095	Q93095 hmo sapien
9	11	2.4	292	4 Q8N4S3	Q8N4S3 hmo sapien
10	11	2.4	471	5 Q9Y1X6	Q9Y1X6 ephydadia f
11	11	2.4	799	4 Q9P0U2	Q9P0U2 hmo sapien
12	11	2.4	802	11 Q7TMP9	Q7TMP9 mus musculus
13	11	2.4	849	11 Q9JLJ8	Q9JLJ8 mus musculus
14	11	2.4	1104	3 Q9P664	Q9P664 neurospora
15	10	2.2	248	4 Q9N8F5	Q9N8F5 hmo sapien
16	10	2.2	340	10 Q6S190	Q6S190 arabidopsis

17	10	2.2	340	10	Q82656
18	10	2.2	382	11	Q63745
19	10	2.2	438	11	Q64642
20	10	2.2	508	13	Q90YJ5
21	10	2.2	582	11	Q64696
22	10	2.2	597	13	Q91871
23	10	2.2	694	13	Q91870
24	10	2.2	694	13	Q7ZYN2
25	10	2.2	775	11	Q80UM4
26	10	2.2	857	13	Q90YJ4
27	10	2.2	872	4	Q86XU4
28	10	2.2	986	4	Q9Y4I9
29	10	2.2	998	4	Q9Y4I6
30	10	2.2	1042	4	Q9Y4F8
31	10	2.2	1191	4	Q7Z3X4
32	10	2.2	1399	4	Q75870
33	10	2.2	1437	5	Q44329
34	10	2.2	1499	13	Q90815
35	10	2.2	1501	11	Q9QW00
36	10	2.2	1501	11	Q7TTL7
37	10	2.2	1502	4	Q8UM81
38	10	2.2	1788	13	Q9IAJ0
39	10	2.2	1863	11	Q64605
40	10	2.2	1887	11	Q9QW67
41	10	2.2	1896	13	Q9IAJ1
42	10	2.2	1898	11	Q9EQI7
43	10	2.2	1898	11	Q64604
44	10	2.2	1904	11	Q64699
45	10	2.2	2051	5	Q44328

ALIGNMENTS

RESULT 1

ID Q7Z637 PRELIMINARY; PRT; 351 AA.

AC Q7Z637; Q7Z637

DT 01-OCT-2003 (TRENBLrel. 25, Created)

DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE PTPN18 protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph;

RX MEDLINE=2338257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Griewood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywicki M.I., Skalska U., Smallus D.E., Schnerch A., Schain J.E.,

RT Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymph;

RA Strausberg R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC052800; AAH52800.1; -.
 SQ SEQUENCE 351 AA; 38317 MW; 5FE9B48C5D0667C4 CRC64;

Query Match 47.4%; Score 217; DB 4; Length 351;
 Best Local Similarity 100.0%; Pred. No. 5.2e-213;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 KRCERYWAQOEPLQTLGFCITLKEKWLNEIMRLTKVTFKESRSYVQLYGMSWPR 198
 DB |||||
 QY 32 KRCERYWAQOEPLQTLGFCITLKEKWLNEIMRLTKVTFKESRSYVQLYGMSWPR 91
 DB |||||
 QY 199 GVPSSPDHMLAWVEARRLQSGPEPLCVHCSAGCGRTGVLCTVDYVYRQLLITQMIIPDP 258
 DB |||||
 QY 92 GVPSSPDHMLAWVEARRLQSGPEPLCVHCSAGCGRTGVLCTVDYVYRQLLITQMIIPDP 151
 DB |||||
 QY 259 SLFDVVLKMRKORPAAVQTEQYRFLYHTVAQMFCSLQNASPHYQNIKENCAPLYDDAL 318
 DB |||||
 QY 152 SLFDVVLKMRKORPAAVQTEQYRFLYHTVAQMFCSLQNASPHYQNIKENCAPLYDDAL 232
 DB |||||

QY 319 FLRTPQALLAIPRPPGGVLRISVPGSPGHAMADTYA 355
 DB |||||

RESULT 2
 ID Q8TA96 PRELIMINARY; PRT; 372 AA.
 AC Q8TA96;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to protein tyrosine phosphatase, non-receptor type 18
 DE (Brain-derived) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RC TISSUE=Lymph, and Lymphoma;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC024280; AAH24280.1; -.
 DR EMBL; BC041562; AAH41562.1; -.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00194; PTPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
 DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_ptp; 1.
 DR Hydrolase; Receptor.
 KW NON_TYR
 RP SEQUENCE 372 AA; 40708 MW; 417CA80AA054CF8B CRC64;

Query Match 47.4%; Score 217; DB 4; Length 372;
 Best Local Similarity 100.0%; Pred. No. 5.4e-213;
 Matches 217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 139 KRCERYWAQOEPLQTLGFCITLKEKWLNEIMRLTKVTFKESRSYVQLYGMSWPR 198
 DB |||||
 QY 53 KRCERYWAQOEPLQTLGFCITLKEKWLNEIMRLTKVTFKESRSYVQLYGMSWPR 112
 DB |||||
 QY 199 GVPSSPDHMLAWVEARRLQSGPEPLCVHCSAGCGRTGVLCTVDYVYRQLLITQMIIPDP 258
 DB |||||
 QY 113 GVPSSPDHMLAWVEARRLQSGPEPLCVHCSAGCGRTGVLCTVDYVYRQLLITQMIIPDP 172
 DB |||||

QY 259 SLFDVVLKMRKORPAAVQTEQYRFLYHTVAQMFCSLQNASPHYQNIKENCAPLYDDAL 318
 DB |||||
 QY 173 SLFDVVLKMRKORPAAVQTEQYRFLYHTVAQMFCSLQNASPHYQNIKENCAPLYDDAL 232
 DB |||||
 QY 319 FLRTPQALLAIPRPPGGVLRISVPGSPGHAMADTYA 355
 DB |||||
 QY 233 FLRTPQALLAIPRPPGGVLRISVPGSPGHAMADTYA 269
 DB |||||

RESULT 3

Q922E3 PRELIMINARY; PRT; 453 AA.
 ID Q922E3
 AC Q922E3;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Similar to protein tyrosine phosphatase, non-receptor type 18.
 DE PTPN18.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC008512; AAH08512.1; -.
 DR MGD; MGI:108410; Ptpn18.
 DR GO; GO:0005737; C:cytoplasm; IEA.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0004726; F:non-membrane spanning protein tyrosine phosphatase.
 DR InterPro; IPR000387; TYR_phosphatase.
 DR InterPro; IPR000242; Tyr_PP.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR SMART; SM00194; PTPC; 1.
 DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
 DR PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_ptp; 1.
 DR Hydrolase; Receptor.
 KW HYDROLASE; RECEPTOR.
 RP SEQUENCE 453 AA; 50227 MW; 722FDE1FFC9F4689 CRC64;

Query Match 7.0%; Score 32; DB 11; Length 453;
 Best Local Similarity 100.0%; Pred. No. 1.3e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AYIATQGPLPHTLLDFWELVWFGVKVILMAC 131
 DB |||||
 QY 100 AYIATQGPLPHTLLDFWELVWFGVKVILMAC 131
 DB |||||

RESULT 4
 Q61152 PRELIMINARY; PRT; 453 AA.
 ID Q61152
 AC Q61152; Q62404;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Protein-tyrosine phosphatase 18 (EC 3.1.3.48) (PTP-K1) (Fetal liver phosphatase 1) (FLP1) (PTP 49) (PTP HSCF).
 DE PTPN18 OR PTPK1.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheng J., Daimaru L., Fennie C., Lasky L.A.;
 RT "A novel protein tyrosine phosphatase expressed in lin(10)CD34(hi)Sca(hi) hematopoietic progenitor cells.";

Query Match 7.0%; Score 32; DB 11; Length 453;
 Best Local Similarity 100.0%; Pred. No. 1.3e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AYIATQGPLPHTLLDFWELVWFGVKVILMAC 131
 DB |||||
 QY 100 AYIATQGPLPHTLLDFWELVWFGVKVILMAC 131
 DB |||||

RESULT 4
 Q61152 PRELIMINARY; PRT; 453 AA.
 ID Q61152
 AC Q61152; Q62404;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Protein-tyrosine phosphatase 18 (EC 3.1.3.48) (PTP-K1) (Fetal liver phosphatase 1) (FLP1) (PTP 49) (PTP HSCF).
 DE PTPN18 OR PTPK1.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheng J., Daimaru L., Fennie C., Lasky L.A.;
 RT "A novel protein tyrosine phosphatase expressed in lin(10)CD34(hi)Sca(hi) hematopoietic progenitor cells.";

Query Match 7.0%; Score 32; DB 11; Length 453;
 Best Local Similarity 100.0%; Pred. No. 1.3e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AYIATQGPLPHTLLDFWELVWFGVKVILMAC 131
 DB |||||
 QY 100 AYIATQGPLPHTLLDFWELVWFGVKVILMAC 131
 DB |||||

RESULT 4
 Q61152 PRELIMINARY; PRT; 453 AA.
 ID Q61152
 AC Q61152; Q62404;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Protein-tyrosine phosphatase 18 (EC 3.1.3.48) (PTP-K1) (Fetal liver phosphatase 1) (FLP1) (PTP 49) (PTP HSCF).
 DE PTPN18 OR PTPK1.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheng J., Daimaru L., Fennie C., Lasky L.A.;
 RT "A novel protein tyrosine phosphatase expressed in lin(10)CD34(hi)Sca(hi) hematopoietic progenitor cells.";

Query Match 7.0%; Score 32; DB 11; Length 453;
 Best Local Similarity 100.0%; Pred. No. 1.3e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AYIATQGPLPHTLLDFWELVWFGVKVILMAC 131
 DB |||||
 QY 100 AYIATQGPLPHTLLDFWELVWFGVKVILMAC 131
 DB |||||

RESULT 4
 Q61152 PRELIMINARY; PRT; 453 AA.
 ID Q61152
 AC Q61152; Q62404;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Protein-tyrosine phosphatase 18 (EC 3.1.3.48) (PTP-K1) (Fetal liver phosphatase 1) (FLP1) (PTP 49) (PTP HSCF).
 DE PTPN18 OR PTPK1.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheng J., Daimaru L., Fennie C., Lasky L.A.;
 RT "A novel protein tyrosine phosphatase expressed in lin(10)CD34(hi)Sca(hi) hematopoietic progenitor cells.";

Query Match 7.0%; Score 32; DB 11; Length 453;
 Best Local Similarity 100.0%; Pred. No. 1.3e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AYIATQGPLPHTLLDFWELVWFGVKVILMAC 131
 DB |||||
 QY 100 AYIATQGPLPHTLLDFWELVWFGVKVILMAC 131
 DB |||||

RESULT 4
 Q61152 PRELIMINARY; PRT; 453 AA.
 ID Q61152
 AC Q61152; Q62404;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Protein-tyrosine phosphatase 18 (EC 3.1.3.48) (PTP-K1) (Fetal liver phosphatase 1) (FLP1) (PTP 49) (PTP HSCF).
 DE PTPN18 OR PTPK1.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheng J., Daimaru L., Fennie C., Lasky L.A.;
 RT "A novel protein tyrosine phosphatase expressed in lin(10)CD34(hi)Sca(hi) hematopoietic progenitor cells.";

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RN Blood 88:1156-1167(1996).
RP [2]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;
RA MEDLINE=97030045; PubMed=8875997;
RA Huang K., Sommers C.L., Grinberg A., Kozak C.A., Love P.E.;
RT "Cloning and characterization of PTP-Ki, a novel nonreceptor protein
RL tyrosine phosphatase highly expressed in bone marrow.";
RL Oncogene 13:1567-1573(1996).
RP [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=C57BL/6; TISSUE=FETAL LIVER;
EX MEDLINE=97131769; PubMed=977243;
RA Dosil M., Leibman N., Lemischka I.R.;
RT "Cloning and characterization of fetal liver phosphatase 1, a nuclear
RL protein tyrosine phosphatase isolated from hematopoietic stem cells.";
RL Blood 88:4510-4525(1996).
CC -!- FUNCTION: MAY BE INVOLVED IN GROWTH AND DIFFERENTIATION OF
CC HEMATOPOIETIC CELLS.
CC -!- CATALYTIC ACTIVITY: PROTEIN TYROSINE PHOSPHATE + H(2)O = PROTEIN
CC TYROSINE + PHOSPHATE.
CC -!- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=FLPIA;
CC IsoId=061152-1; Sequence=Displayed;
CC Name=FLPIB;
CC IsoId=061152-2; Sequence=VSP_050405;
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN BONE MARROW. ALSO
CC EXPRESSED IN KIDNEY, LUNG, OVARY, SPLEEN, THYMUS AND LYMPH NODE.
CC -!- DEVELOPMENTAL STAGE: EXPRESSED IN THE EMBRYO FROM DAY 15.5.
CC -!- SIMILARITY: BELONGS TO THE NON-RECEPTOR CLASS OF THE PROTEIN-
CC TYROSINE PHOSPHATASE FAMILY.
DR EMBL; U35124; AB82736.1; -.
DR EMBL; U49853; AB18623.1; -.
DR EMBL; U52523; AAC52991.1; -.
DR HSSP; Q06124; 2SHP.
DR MGD; MGI:108410; Ptpn18.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR GO; GO:0005634; C:nucleus; IDA.
DR GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . . ; IDA.
DR InterPro; IPR000387; TYR_PP.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
DR DOVAIN 56 PROTEIN-TYROSINE PHOSPHATASE.
DR DOVAIN 312 428 PRO/SER/THR-RICH.
DR ACT_SITE 229 229 BY SIMILARITY.
DR VARSPIC 9 32 Missing (in isoform FLPIB).
FT FTId=VSP_050405.
FT CONFLICT 11 11 F -> L (IN REF. 3).
FT CONFLICT 362 368 ASAGTGP -> LRHRA (IN REF. 3).
SQ SEQUENCE 453 AA; 50201 MW; 88AD7E73CE8136B0 CRC64;

Query Match 7.0%; Score 32; DB 11; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 AYIATQGPLPHTLLDFWELVWVFGVKVILMAC 131
D5 [|||||]
D5 100 AYIATQGPLPHTLLDFWELVWVFGVKVILMAC 131

RESULT 5
P70602 ID P70602 PRELIMINARY; PRT; 453 AA.
AC P70602;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
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DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Protein tyrosine phosphatase 20.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97067206; PubMed=8910608;
RA Aoki N., Yamaguchi-Aoki Y., Ullrich A.;
RT "The novel protein-tyrosine phosphatase PTP20 is a positive regulator
of PC12 cell neuronal differentiation.";
RL J. Biol. Chem. 271:29422-29426(1996).
RP [2]
RP SEQUENCE FROM N.A.
RA Aoki N., Yamaguchi-Aoki Y., Ullrich A.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U69673; AAC52896.1; -.
DR HSSP; Q06124; 2SHP.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS50056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.
DR Hydrolase.
KW HYDROLASE.
SQ SEQUENCE 453 AA; 50106 MW; 6CCC132206FB69AE CRC64;

Query Match 6.3%; Score 29; DB 11; Length 453;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 430 GAQTGGLGFNLRIGRPKGRPPPAEWTRV 458
D5 [|||||]
D5 425 GAQTGGLGFNLRIGRPKGRPPPAEWTRV 453

RESULT 6
Q90Y62 ID Q90Y62 PRELIMINARY; PRT; 258 AA.
AC Q90Y62;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Receptor PTP-like protein IA-2 (Fragment).
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21076097; PubMed=11206415;
RA Cai T., Krause M.W., Odenwald W.F., Toyama R., Notkins A.L.;
RT "The IA-2 gene family: homologs in Caenorhabditis elegans, Drosophila
and zebrafish.";
RL Diabetologia 44:81-88(2001).
DR EMBL; AF190144; AAL05974.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
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DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydroxylase.
FT NON TER
SQ SEQUENCE 258 AA; 29544 MW; 93FBC53CAA4EA4A2 CRC64;
Query Match 2.6%; Score 12; DB 13; Length 258;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 AYIATQGLPHT 111
Db 58 AYIATQGLPHT 69

RESULT 7
ID Q9NL13 PRELIMINARY; PRT; 487 AA.
AC Q9NL13;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE AMTPR4C protein (Fragment).
GN AMTPR4C.
OS Branchiostoma belcheri (Amphioxus).
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7741;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20219325; PubMed=10754074;
RA Ono-Koyanagi K., Suga H., Katch K., Miyata T.;
RT "Protein tyrosine phosphatases from amphioxus, hagfish, and ray:
RT divergence of tissue-specific isoform genes in the early evolution of
RT vertebrates.";
RL J. Mol. Evol. 50:302-311 (2000).
DR EMBL; AB033564; BAA95171.1; -.
DR HSSP; P18052; 1YFO.
DR GO; GO:0016787; F:Hydrolase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_PP.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 2.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 2.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 2.
KW Hydroxylase.
FT NON TER
SQ SEQUENCE 487 AA; 55573 MW; CF2BCC6D933C6ADD CRC64;
Query Match 2.6%; Score 12; DB 5; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 AYIATQGLPHT 111
Db 267 AYIATQGLPHT 278

RESULT 8
ID Q93095 PRELIMINARY; PRT; 84 AA.
AC Q93095;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Protein tyrosine phosphatase PEP (EC 3.1.3.48) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Dayon M.A., Knodloch T.J.;
RT "Multiple phosphotyrosine phosphatase mRNAs are expressed in the human
RT lung fibroblast cell line WI-38.";
RL Submitted (SEP-1996) to the EMBL/GenBank/DBSJ databases.
DR EMBL; U69700; AAB09079.1; -.
DR HSSP; P29350; 1GWZ.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004727; F:phosphorylated protein tyrosine phosphatase act. .; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydroxylase.
FT NON TER
SQ SEQUENCE 84 AA; 9699 MW; 4DA40B7BA38E45DA CRC64;
Query Match 2.4%; Score 11; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 0.0089;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 228 HCSAGCGRTGV 238
Db 67 HCSAGCGRTGV 77

RESULT 9
ID Q8N4S3 PRELIMINARY; PRT; 292 AA.
AC Q8N4S3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Renal adenocarcinoma;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC033716; AAH33716.1; -.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR003595; PTPC motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC motif; 1.
DR PROSITE; PS00215; MITOCH CARRIER; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hypothetical protein.
FT NON TER
SQ SEQUENCE 292 AA; 33121 MW; 54B838BDD41D1BD7 CRC64;
Query Match 2.4%; Score 11; DB 4; Length 292;

```


Best Local Similarity 100.0%; Pred. No. 0.027; Mismatches 0; Indels 0; Gaps 0; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 KNRYKDVLPYD 69
Dd 52 KNRYKDVLPYD 62

RESULT 10

Q9YIX6 PRELIMINARY; PRT; 471 AA.
AC Q9YIX6;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE SPTRP4 (Fragment).
OS Ephydriata fluviatilis.
OC Eukaryota; Metazoa; Porifera; Demospongiae; Ceractinomorpha;
OC Haplosclerida; Spongillidae; Ephydria.
OX NCBI_TaxID=31330;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9246376; PubMed=1029569;
RA Ono K., Suga H., Iwabe N., Kuma K., Miyata T.;
RT "Multiple protein tyrosine phosphatases in sponges and explosive gene
RT duplication in the early evolution of animals before the parazoan-
RT eumetazoan split.";
EL J. Mol. Evol. 48:654-662(1999).
DR HSSP; AB019125; BRA82558.1; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 2.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 2.
DR PROSITE; PS0056; TYR_PHOSPHATASE 2; 2.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 2.
KW Hydrolase.
FT NON_TER
SQ SEQUENCE 471 AA; 54509 MW; 7DA6245615A6A56 CRC64;

Query Match 2.4%; Score 11; DB 5; Length 471;
Best Local Similarity 100.0%; Pred. No. 0.042; Mismatches 0; Indels 0; Gaps 0; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCAGCGRTG 237
Dd 399 VHCAGCGRTG 409

RESULT 11

Q9POU2 PRELIMINARY; PRT; 799 AA.
AC Q9POU2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Protein tyrosine phosphatase.
GN PTP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RA Huang C., Zhang C., Wu T., Peng Y., Gu Y., Zhang L., Jiang C., Li Y.,
RA Han Z., Wang Y., Chen Z., Fu G.;
RT "A novel gene expressed in human adrenal gland.";

Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

EMBL; AF150732; AAF67472.1; -.
HSSP; Z29350; IGMZ.
GO; GO:0016787; F:hydrolase activity; IEA.
GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; TYR_PP.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHPTASE.
SMART; SM00194; PTPC; 1.
PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
PROSITE; PS0056; TYR_PHOSPHATASE 2; 1.
PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 799 AA; 90610 MW; 93F5385016F33D0C CRC64;

Query Match 2.4%; Score 11; DB 4; Length 799;
Best Local Similarity 100.0%; Pred. No. 0.067; Mismatches 0; Indels 0; Gaps 0; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 228 HCSAGCGRTG 238
Dd 226 HCSAGCGRTG 236

RESULT 12

Q7TMP9 PRELIMINARY; PRT; 802 AA.
AC Q7TMP9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCT; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci R., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCT; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055377; AAH55377.1; -.
KW Receptor.
SQ SEQUENCE 802 AA; 89694 MW; BB8C3AA618B28561 CRC64;

Query Match 2.4%; Score 11; DB 11; Length 802;
Best Local Similarity 100.0%; Pred. No. 0.067;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 228 HCSAGCGRTG 238
| | | | | | | | | |
Db 226 HCSAGCGRTG 236

RESULT 13

Q9JLJ8 PRELIMINARY; PRT; 849 AA.

AC Q9JLJ8
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE PTP36-B isoform.
GN PTPN14.

OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=DDY;
RX MEDLINE=20068798; PubMed=10600535;
RA Aoyama K., Matsuda T., Aoki N.;
RT "Characterization of newly identified four isoforms for a putative
RT cytosolic protein tyrosine phosphatase PTP36.";
EL Biochem Biophys Res Commun. 266:523-531(1999).
DR EMBL; AF170903; AA27549.1; -.
DR HSP; Q06124; 2SHP.
DR MG; MG1:102467; C:cytoskeleton; IEA.
DR GO; GO:0005856; C:cytoskeleton; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000299; Band 4.1.
DR InterPro; IPR000387; TYR_PTPase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00373; Band 41; 1.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00935; BAND41.
DR PRINTS; PR00700; PRTYPHTASE.
DR SMART; SM00295; B41; 1.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00660; FERM_1; 1.
DR PROSITE; PS00661; FERM_2; 1.
DR PROSITE; PS00057; FERM_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 849 AA; 97656 MW; 4945441F3F00B4EE CRC64;

Query Match 2.4%; Score 11; DB 11; Length 849;
Best Local Similarity 100.0%; Pred. No. 0.071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 YIATQGLPHT 111
| | | | | | | | | |
Db 641 YIATQGLPHT 651

RESULT 14

Q9P664 PRELIMINARY; PRT; 1104 AA.

AC Q9P664
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Related to protein-tyrosine-phosphatase.
GN B104.180.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;

OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RA Schulte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL35928; CAB91306.2; -.
DR HSP; P29350; 1GWZ.
DR GO; GO:0005743; C:mitochondrial inner membrane; IEA.
DR GO; GO:0005488; F:binding; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR001993; Mitoch carrier.
DR InterPro; IPR001763; Rhodanese-like.
DR InterPro; IPR000387; TYR_PTPase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHTASE.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00450; RHOD; 1.
DR PROSITE; PS00215; MITOCH CARRIER; 1.
DR PROSITE; PS00206; RHODANESE_3; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 1104 AA; 120371 MW; 5D25498BCFF7FF22 CRC64;

Query Match 2.4%; Score 11; DB 3; Length 1104;
Best Local Similarity 100.0%; Pred. No. 0.09;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 227 VHCAGCGRTG 237
| | | | | | | | | |
Db 904 VHCAGCGRTG 914

RESULT 15

Q9NSR5 PRELIMINARY; PRT; 248 AA.

AC Q9NSR5
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP761A0712.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Amalgam;
RA Ansoorge W., Winkler U., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL157451; CAB75665.1; -.
DR PIR; T46903; T46903.
DR HSP; P29350; 1GWZ.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_PTPase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHTASE.
DR SMART; SM00194; PTPC; 1.

DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hypothetical protein; Hydrolase.
FT NON TER 1
SQ SEQUENCE 248 AA; 28304 MW; EE10C57FBC5B5114 CRC64;
Query Match 2.2%; Score 10; DB 4; Length 248;
Best Local Similarity 100.0%; Pred.No. 0.25;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 100 AYIATQGGLP 109
Db 48 AYIATQGGLP 57
Search completed: August 17, 2004, 20:52:34
Job time : 49 secs

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Sequence 12, Appl
Sequence 38, Appl
Sequence 2, Appl
Sequence 21, Appl
Sequence 21, Appl
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Sequence 2, Appl
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Sequence 37, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 19, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 5, Appl

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29 448.5 18.5 232 2 US-08-446-345-38
30 448 18.5 913 4 US-09-848-294-2
31 441.5 18.2 242 2 US-08-685-992-21
32 441.5 18.2 242 2 US-09-144-925-21
33 435 17.9 1337 3 US-08-854-585-2
34 435 17.9 1337 4 US-09-447-533-2
35 435 17.9 1337 5 PCT-US95-05512-2
36 433 17.9 244 4 US-08-848-294-7
37 429.5 17.7 278 1 US-08-201-697-16
38 429 17.7 231 2 US-08-446-345-37
39 426.5 17.6 802 1 US-08-015-985-1
40 426.5 17.6 802 4 US-09-280-597-1
41 426 17.6 258 2 US-08-685-992-19
42 426 17.6 258 2 US-09-144-925-19
43 424.5 17.5 385 1 US-08-036-210-5
44 424.5 17.5 385 2 US-08-449-609-5
45 424.5 17.5 385 4 US-09-361-096A-5

ALIGNMENTS

RESULT 1
US-08-821-278A-2
; Sequence 2, Application US/08821278A
; Patent No. 6238902
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; NUMBER OF SEQ ID NOS: 23
; SEQ ID NO 2
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Mus Musculus
US-08-821-278A-2

Query Match 73.4%; Score 1778.5; DB 3; Length 453;
Best Local Similarity 74.9%; Pred. NO. 7.9e-154;
Matches 344; Conservative 32; Mismatches 76; Indels 7; Gaps 2;

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DB 1 MSRLDLSRSLERLEARGREGVLAAGEFSDIQASAAKADGVCSVTAGSRPENVRKN 60
QY 61 RYKDVLPYDQTRVILSLQEEHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
DB 61 RYKDVVAYDETRVILSLQEEHSDYINGNFIRGVDGSLAYIATQGPLPHTLLDFWRLVW 120
QY 121 EFGVKVILMACREIENGRCRYWAQCEPLQTLGFCITLIKEXWLNEDIMRLTKVTF 180
DB 121 EFGVKVILMACREIENGRCRYWAQCEPLQTLGFCITLIKEXWLNEDIMRLTKVTF 180
QY 181 QXESRSVYQLOQWSPDRGVPSDDHMLAMVEEARLQSGPEPLCHVCSAGCGRTGVLC 240
DB 181 QXESRSVYQLOQWSPDRGVPSDDHMLAMVEEARLQSGPEPLCHVCSAGCGRTGVLC 240
QY 241 TVDYVRQLLLTQMIPDFSLFDVYLKMKQKPAAVQTEQRYFLYHTVAQFPCSTLQNAS 300
DB 241 AVDYVRQLLLTQMIPDFSLFDVYLKMKQKPAAVQTEQRYFLYHTVAQFPCSTLQNAS 300
QY 301 PHYQNKENCAPLYDDALFLRTPQALLAIPRPPGGVLSISVPGSPGHAMADTYAEOKR 360
DB 301 PHYQNKENCAPLYDDALFLRTPQALLAIPRPPGGVLSISVPGSPGHAMADTYAEOKR 360
QY 361 GAPAGAGSGTGTGTGARSAAEAPLYSKVTPRAQPGAHAEADAGTLP-GRVPAQDQSPA 419
DB 361 GASAGTGPGRAPTST-----DTPIYSQVAPRAQRPVAHTEDAQGTALRRVPADQSS 414

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OM protein - protein search, using sw model

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Searched: 389414 seqs, 51625971 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778.5	73.4	453	3	US-08-821-278A-2
2	1754.5	72.4	453	3	US-08-951-260A-7
3	1754.5	72.4	453	3	US-08-430-626A-7
4	830	34.2	155	3	US-08-821-278A-17
5	755.5	31.2	802	3	US-08-081-345-18
6	727.5	30.0	807	3	US-08-081-345-2
7	715.5	29.5	278	3	US-08-821-278A-18
8	695	28.7	272	3	US-08-821-278A-19
9	665	27.4	253	2	US-08-685-992-20
10	665	27.4	253	2	US-08-144-925-20
11	493.5	20.4	255	2	US-08-685-992-16
12	493.5	20.4	255	2	US-08-144-925-16
13	474	19.6	1711	2	US-08-342-930-2
14	467	19.3	595	1	US-08-202-389-6
15	465	19.2	631	1	US-08-202-389-8
16	463.5	19.1	277	2	US-08-685-992-22
17	463.5	19.1	277	2	US-08-144-925-22
18	463.5	19.1	513	1	US-08-202-389-2
19	463	19.1	843	4	US-09-417-197-117
20	463	19.1	853	4	US-09-417-197-119
21	461	19.0	593	1	US-08-018-129-5
22	461	19.0	593	4	US-08-448-250-5
23	461	19.0	593	4	US-09-282-257-5
24	456	18.8	263	2	US-08-685-992-13
25	456	18.8	263	2	US-09-144-925-13
26	454	18.7	266	2	US-08-685-992-12
27	454	18.7	266	2	US-08-144-925-12

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QY 420 GSGAYEDVAGGAGTGGGGLGNLRIGRPGKPRDPPPAEWTRV 458
DB 415 GPDAYEEVTDGAQTGGGLGNLRIGRPGKPRDPPPAEWTRV 453

RESULT 2
US-08-951-260A-7
; Sequence 7, Application US/08951260A
; Patent No. 6004791
; GENERAL INFORMATION:
; APPLICANT: Aoki, Naohito
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
; TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/951,260A
; FILING DATE: October 16, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,860
; FILING DATE: No. 6004791ember 13, 1996
; APPLICATION NUMBER: PCT/1897/00946
; FILING DATE: June 17, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 227/004
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-951-260A-7

Query Match 72.4%; Score 1754.5; DB 3; Length 453;
Best Local Similarity 74.5%; Pred. No. 1.2e-151;
Matches 342; Conservative 37; Mismatches 73; Indels 7; Gaps 3;

QY 1 MSRLDSARSFLEKLEARGREGAVLAGESDIOACSAWAKDGVCSVAGSPENVRKN 60
DB 1 MSRQSDLVRSFLQEQEARDKGAILAREFSDIKARSVAMKTEGVCSTKAGSQGSKKN 60
QY 61 RYKDLVPYDTRVLSLLQEGHSDYINGNFIKGVDSGLAYIATQGPLHTLLDFRLVW 120
DB 61 RYKDVVPYDTRVLSLLQEGHSDYINGNFIKGVDSGLAYIATQGPLHTLLDFRLVW 120
QY 121 EFGVKVILMACREIENGKRCERYWAOBPLQTLGFCITLKEKWNEDIMRLTKVTF 180
DB 121 EFGIKVILMACQETENGRRRCERYWAOBPLQAGPFCITLTETALTSITLTLQVTF 180
QY 181 QKBSRSYVQLQYMSWPDGRGVPSSPDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVL 240
DB 181 QKESRPVQLQYMSWPDHGVSPSSSDHILTMVEEARCLQGLGFLCVHCSAGCGRTGVL 240

QY 241 TDVYVRLQLLTQMLPPDPFSLFDVLMKMKORPAAVQTEEQYRFLYHTVAQMFCSTLQNAS 300
DB 241 ADVYVRLQLLTQTPPNFSLFEVLEMKRQBPAAVQTEEQYRFLYHTVAQLFSTLQNAS 300
QY 301 PHYQNIKENCAPLYDDALFLRTPOALLAIPRPPGVLRSISVPCSPGHAMADTYAEQKR 360
DB 301 PLYQNLKENRAPICKDSSSLRTSSALPATSRPLGVLRSISVPCPPTLPNADTYAVVQKR 360
QY 361 GAPAGAGSGTGTGTGARSAAEAPLYSKVTPRAORPCAAHAEDARGTLP-CRVPADQSPA 419
DB 361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHSTENAQGTTLGRVPADENPS 414
QY 420 GSGAYEDVAGGAGTGGGGLGNLRIGRPGKPRDPPPAEWTRV 458
DB 415 GPDAYEEVTDGAQTGGGLGNLRIGRPGKPRDPPPAEWTRV 453

RESULT 3
US-09-430-626A-7
; Sequence 7, Application US/09430626A
; Patent No. 6482605
; GENERAL INFORMATION:
; APPLICANT: Aoki, Naohito
; APPLICANT: Ullrich, Axel
; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
; TITLE OF INVENTION: AND RELATED PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/430,626A
; FILING DATE: 29-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/951,260
; FILING DATE: October 16, 1997
; APPLICATION NUMBER: 60/030,860
; FILING DATE: No. 6482605ember 13, 1996
; APPLICATION NUMBER: PCT/1897/00946
; FILING DATE: June 17, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 227/004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
; US-09-430-626A-7

Query Match 72.4%; Score 1754.5; DB 4; Length 453;

```

Best Local Similarity 74.5%; Pred. No. 1.2e-151;
Matches 342; Conservative 37; Mismatches 73; Indels 7; Gaps 3;
QY 1 MSRLDARGFLERLEARGREGAVLAGESDIOACSAAMKADGVCSTVAGSPENVRKN 60
DB 1 MSQSDLVRFLEQOEARDKGAILEAREFSDIKARVANKTEGVSTKAGSQGHSKN 60
QY 61 RYKDVLPYDQTRVLSLLOEGHSDYINGNPIRGVDSGLAYIATQGPLPHTLLDFWRLVW 120
DB 61 RYKDVLPYDQTRVLSLLOEGHSDYINGNPIRGVDSGLAYIATQGPLPHTLLDFWRLVW 120
QY 121 EFGVKVILMACRETEGRKCECERWAOEPLQTLGFCITLKEKWLNEDIMLRTLVTP 180
DB 121 EFGVKVILMACRETEGRKCECERWAOEPLQTLGFCITLKEKWLNEDIMLRTLVTP 180
QY 181 QKESRSYQLOQYMSWPDGRGVPSSPDHMLAMVEARLQSGPPEPLCVHCSAGCGRTGVLC 240
DB 181 QKESRPVHQLOQYMSWPDGRGVPSSPDHMLAMVEARLQSGPPEPLCVHCSAGCGRTGVLC 240
QY 241 TVDYVROLITLQMTIPPDSFLFDVVLKVRKORPAAVQTEBQYRFLYHTVAQMFCSSTLQNAS 300
DB 241 AVDYVROLITLQMTIPPDSFLFDVVLKVRKORPAAVQTEBQYRFLYHTVAQMFCSSTLQNAS 300
QY 301 PHYNIKENCAPLYDDALFRTPCALLAI PRPPGGVLRISVPGSPGHAMADTYAEQKR 360
DB 301 FLIQNLKENAPICKDSSRLTSALPATSRPLGGVLRISVPGPPTLPMADTYAVVQKR 360
QY 361 GAPAGAGSGTGTGTGARGAERAPLYSKYTPRAQPGAHAEARGTLP-GRVPADQSPA 419
DB 361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTEAQAQGTALGRVPADENPS 414
QY 420 GSGAYEDVAGCAOTGGGLGENLRIGRPGKPRDPAETRV 458
DB 415 GPDAYEETDCAOTGGGLGFNLRIGRPGKPRDPAETRV 453
RESULT 4
US-08-821-278A-17
; Sequence 17, Application US/08821278A
; Patent No. 6238502
; GENERAL INFORMATION:
; APPLICANT: Cheng, Jill
; APPLICANT: Lasky, Laurence A.
; TITLE OF INVENTION: Protein Tyrosine Phosphatases
; FILE REFERENCE: P1010R1
; CURRENT APPLICATION NUMBER: US/08/821,278A
; CURRENT FILING DATE: 1997-03-20
; SEQ ID NO 17
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Homo Sapien
US-08-821-278A-17
Query Match 34.2%; Score 830; DB 3; Length 155;
Best Local Similarity 100.0%; Pred. No. 5.5e-68;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 ARGREGAVLAGESDIOACSAAMKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVLS 76
DB 1 ARGREGAVLAGESDIOACSAAMKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVLS 60
QY 77 LLOEGHSDYINGNPIRGVDSGLAYIATQGPLPHTLLDFWRLVWVEFGVKVILMACREIEN 136
DB 61 LLOEGHSDYINGNPIRGVDSGLAYIATQGPLPHTLLDFWRLVWVEFGVKVILMACREIEN 120
QY 137 GRKRCERYWAOEPLQTLGFCITLKEKWLNEDI 171
DB 121 GRKRCERYWAOEPLQTLGFCITLKEKWLNEDI 155
RESULT 5
US-09-081-345-18

; Sequence 18, Application US/09081345
; Patent No. 6228641
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; APPLICANT: Gregory D. Plozman
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; TITLE OF INVENTION: PTP04 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSeq for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/081,345
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/047,222
; FILING DATE: May 20, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/253
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 802 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-081-345-18
Query Match 31.2%; Score 755.5; DB 3; Length 802;
Best Local Similarity 44.0%; Pred. No. 3.6e-60;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;
QY 27 AGEPSDIOACSAAMKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVLSLLOEGHSDY 86
DB 25 ASEFLKLRQSTKYKADKIYPTVAORPKNKRYKDIILPYDHSLSLTTDESSY 84
QY 87 INGNPIRGVDSGLAYIATQGPLPHTLLDFWRLVWVEFGVKVILMACREIENGKRCERYWA 146
DB 85 INASPIKGYGPKAYIATQGPLSTLLDFWRLVWVEFGVKVILMACREIENGKRCERYWA 144
QY 147 QEOE-PLQTLGFCITLKEKWLNEDIMLRTLVTPFQKESRSYQLOQYMSWPDGRVPS 205
DB 145 EPGTQLOFGPFSISCEAEK-KKSDYKLTIRLAKFNNETRIIYQHYKNWPDHDPSSID 203
QY 206 HMLAMVEARLQSGPPEPLCVHCSAGCGRTGVLCITLKEKWLNEDIMLRTLVTPFQKESRSYQLOQYMSWPDGRVPS 265
DB 204 PLQLIWMRCYQEDDDCVPICHCSAGCGRTGVCAVDYTWMLLKDGIIPKNFSVFNLIQ 263
QY 266 KVRKORPAAVQTEBQYRFLYHTVAQMFCSSTLQNASPHYQNIKENCAPLYDDALFLRTPOA 325
DB 264 EMRTORPSLVQTEBQYELVYSAVLELF-----KREMDVTSNDHLG-----REIQ 308
QY 326 LLAIPRPPGGVLRISVPGS-----PGHAMAD--TVAEOKRGAPAGAGSGTGTGTG 377
DB 309 QCSIFE-----QSLTVZADSCPLDLPKNVRDVKTTNQHSKQGAESSTGSSISGLRTS 362

QY 378 ARSAEE 383

Db 363 TMRAEE 368

RESULT 6

US-09-081-345-2
; Sequence 2, Application US/09081345

; Patent No. 6228641

; GENERAL INFORMATION:

; APPLICANT: Bahija Jallal

; APPLICANT: Gregory D. Plowman

; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF

; TITLE OF INVENTION: PTP04 RELATED DISORDERS

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/081,345

; FILING DATE: Herewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/047,222

; FILING DATE: May 20, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Warburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 234/253

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 807 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-081-345-2

Query Match 30.0%; Score 727.5; DB 3; Length 807;

Best Local Similarity 46.9%; Pred. No. 1.3e-57;

Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;

QY 27 AGEFSDIQACSAANKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVILSLQEEGHSY 86

Db 25 ANEFKLKROSTKYKADKTYPTTVAEPKNIKKNRYKDVLPYDYSRVLSLTSDESSY 84

QY 87 INGNFIRGVDGSLAYIATQGPLHTLLDFWRLVWEFGVKVILMACREIENGKRCERYWA 146

Db 85 INANFIKGVYGPXAYIATQGPLSTLLDFWRMIWEYSVLIIVMACMEYEGKKKERYWA 144

QY 147 QEQP-PLQTGLFCITLKEKWLNEIMRLTKVTFQKESRSVYQLOQYMSWPDGVPSSPD 205

Db 145 EPGEMQLEFGPFPSSCBAEK-RKSDYIIRTLKVKFNSETETIYQFYKXWPDHVPSSID 203

QY 206 HMLAMVEARLQSGPEPLCVHCSAGCGRTGVLTVDYVYRQLLTQMIIPDPSLFDVVL 265

Db 204 PILELIWDVRCYQEDDSDVPICIHCSAGCGRTGVICAIDYTWMLLKDGIIIPNFSVFLIR 263

QY 266 KVRKQRPAAVQTEQRYFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312

Db 264 EMRTQPSLVQTQEQYELVYNVLELFRQMDVIRDKHSGTESQAKHCIP 313

RESULT 7

US-08-821-278A-18

; Sequence 18, Application US/08821278A

; Patent No. 6238902

; GENERAL INFORMATION:

; APPLICANT: Cheng, Jill

; APPLICANT: Lasky, Laurence A.

; TITLE OF INVENTION: Protein Tyrosine Phosphatases

; FILE REFERENCE: P1010R1

; CURRENT APPLICATION NUMBER: US/08/821,278A

; CURRENT FILING DATE: 1997-03-20

; NUMBER OF SEQ ID NOS: 23

; SEQ ID NO 18

; LENGTH: 278

; TYPE: PRT

; ORGANISM: Homo Sapien

US-08-821-278A-18

Query Match 29.5%; Score 715.5; DB 3; Length 278;

Best Local Similarity 48.9%; Pred. No. 3.5e-57;

Matches 139; Conservative 45; Mismatches 91; Indels 9; Gaps 3;

QY 27 AGEFSDIQACSAANKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVILSLQEEGHSY 86

Db 2 ASEFLKLRQSTKYKADKTYPTTVAQRPKNIKKNRYKDVLPYDHSLSLTSDESSY 61

QY 87 INGNFIRGVDGSLAYIATQGPLHTLLDFWRLVWEFGVKVILMACREIENGKRCERYWA 146

Db 62 INASFIKGVYGPXAYIATQGPLSTLLDFWRMIWEYRILVIVMACMEFEGKKKERYWA 121

QY 147 QEQP-PLQTGLFCITLKEKWLNEIMRLTKVTFQKESRSVYQLOQYMSWPDGVPSSPD 205

Db 122 EPGETQLQFGPFPSSCBAEK-KXSDYKIRTLKAKFNNETRIIYQFYKXWPDHVPSSID 180

QY 206 HMLAMVEARLQSGPEPLCVHCSAGCGRTGVLTVDYVYRQLLTQMIIPDPSLFDVVL 265

Db 181 PILELIWDVRCYQEDDSDVPICIHCSAGCGRTGVICAIDYTWMLLKDGIIIPNFSVFLIR 240

QY 266 KVRKQRPAAVQTEQRYFLYHTVAQMFCSSTLQNASPHYQNIKENCAP 309

Db 241 EMRTQPSLVQTQEQYELVYNVLELFRQMDVIRDKHSGTESQAKHCIP 277

RESULT 8

US-08-821-278A-19

; Sequence 19, Application US/08821278A

; Patent No. 6238902

; GENERAL INFORMATION:

; APPLICANT: Cheng, Jill

; APPLICANT: Lasky, Laurence A.

; TITLE OF INVENTION: Protein Tyrosine Phosphatases

; FILE REFERENCE: P1010R1

; CURRENT APPLICATION NUMBER: US/08/821,278A

; CURRENT FILING DATE: 1997-03-20

; NUMBER OF SEQ ID NOS: 23

; SEQ ID NO 19

; LENGTH: 272

; TYPE: PRT

; ORGANISM: Homo Sapien

US-08-821-278A-19

Query Match 28.7%; Score 695; DB 3; Length 272;

Best Local Similarity 47.1%; Pred. No. 2.5e-57;

Matches 128; Conservative 55; Mismatches 87; Indels 2; Gaps 2;

QY 27 AGEFSDIQACSAANKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVILSLQEEGHSY 86

Db 27 AGEFSDIQACSAANKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVILSLQEEGHSY 86

Db 2 ARDFWRLRLSTKYRTEKIYPTATGEKEENVKKNRYKDILPFDHSRVKLTILKTPSQSDY 61
 Qy 97 INGNFIRGVDGLAYIATQGLPHLLDFWRLVWFGVKVILMACREIENGRKRCERYW- 145
 Db 62 INANFIKGVGPKAYVATQGLANTVIDFWMVWYVNVIIWVACREFEMGRKKCERYW 121
 Qy 146 AQEQEPLQGLFCITLILKEKWLNEIDIMRLTKVTFOKESRVYQLQYMSWPDGRGVSSPD 205
 Db 122 LYGEDPITFAFKLS-CEDEQARTDYFIRILLLEFQNESRRLYQFHYVNPDPDHDVSSFD 180
 Qy 206 HMLAMVEARLQSGPEPLCVHCSAGCGRTGVLTVDYVROLTLTQMIPEPDSFLFDVVL 265
 Db 181 SILDMISLMRYQEHEDVPICIHCSAGCGRTGAICAIDYTWNLLKAGKIPEEFNVNLIQ 240
 Qy 266 KRRKQRPAAVQTEQRYRFLVHTVAQMFCSLQ 297
 Db 241 EMRTORHSAVQTEQRYELVHRAIAQLFEKQLQ 272

RESULT 9

US-08-685-992-20
 ; Sequence 20, Application US/08685992
 ; Patent No. 5912138
 ; GENERAL INFORMATION:
 ; APPLICANT: Tonks, Nicholas
 ; APPLICANT: Flint, Andrew J.
 ; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 ; TITLE OF INVENTION: TYROSINE PHOSPHATASES
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/685,992
 ; FILING DATE: 25-JUL-1996
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: CSHL96-03
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 781-861-6240
 ; TELEFAX: 781-861-9540
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 253 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-685-992-20

Query Match 27.4%; Score 665; DB 2; Length 253;
 Best Local Similarity 49.4%; Pred. No. 1.2e-52;
 Matches 126; Conservative 44; Mismatches 73; Indels 12; Gaps 3;
 Qy 48 TVAGSRPENVKRYKDVLPDQTRVILSLQEGHSDYNGNIRGVGDSLAIYATQGP 107
 Db 4 TATGKEENVKKNRYKDILPFDHSRVKLTILKTPSQSDYINANFIKGVGPKAYVATQGP 63

Qy 108 LPHTLLDFWRLVWFGVKVILMACREIENGRKRCERYW-AQEQEPLQGLFCITLILKEKW 166
 Db 64 LANTVIDFWMVWYVNVIIWVACREFEMGRKKCERYWFLYGEDPITFAFKISC----- 118
 Qy 167 LNEIDIMRLT---LKVTFOKESRVYQLQYMSWPDGRGVSSPDHMLAMVEARLQSGSP 222
 Db 119 --EDQARTDYFIRILLLEFQNESRRLYQFHYVNPDPDHDVSSFDLSILMKRYQEHED 176
 Qy 223 EPLCVHCSAGCGRTGVLTVDYVROLTLTQMIPEPDSFLFDVVLKRRKQRPAAVQTEQYR 282
 Db 177 VPICIHCSAGCGRTGAICAIDYTWNLLKAGKIPEEFNVNLIQEMRTORHSAVQTEQYR 236
 Qy 283 FLYHTVAQMFCSLQ 297
 Db 237 LVHRAIAQLFEKQLQ 251

RESULT 10
 US-09-144-925-20
 ; Sequence 20, Application US/09144925
 ; Patent No. 5951979
 ; GENERAL INFORMATION:
 ; APPLICANT: Tonks, Nicholas
 ; APPLICANT: Flint, Andrew J.
 ; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 ; TITLE OF INVENTION: TYROSINE PHOSPHATASES
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02421-4799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: Windows 95
 ; SOFTWARE: FastSEQ for Windows Version 2.0b
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,925
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/685,992
 ; FILING DATE: July 25, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: CSHL96-032
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 781-861-6240
 ; TELEFAX: 781-861-9540
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 20:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 253 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-09-144-925-20

Query Match 27.4%; Score 665; DB 2; Length 253;
 Best Local Similarity 49.4%; Pred. No. 1.2e-52;
 Matches 126; Conservative 44; Mismatches 73; Indels 12; Gaps 3;
 Qy 48 TVAGSRPENVKRYKDVLPDQTRVILSLQEGHSDYNGNIRGVGDSLAIYATQGP 107
 Db 4 TATGKEENVKKNRYKDILPFDHSRVKLTILKTPSQSDYINANFIKGVGPKAYVATQGP 63
 Qy 108 LPHTLLDFWRLVWFGVKVILMACREIENGRKRCERYW-AQEQEPLQGLFCITLILKEKW 166

Db 64 LANTVIDFRWVYVNIIVMACREPFEMGRKCCRYWPLYGDDPITPAFFKISC----- 118
 Qy 167 LNEIDIMRLTKVTFQKESRSYVQLQYMSWPDGRGVPSPPDHMLAMVEBARR-----LQSG 221
 Db 119 --EDEQARTDYFILLBFQNESRRLYQFYVNNWPDHDPSSPFDILDMISLAKRYQEHED 176
 Qy 223 EPLCVHCSAGCGRTGVLCTVDYVYRQLLLTQWIPDFSLFDVVLKMKRKQRPAAVQTEQYR 282
 Db 177 VPICHSAGCGRTGALCAIDYTNWLLKAGKIPEEFNVFNLIQEMRTQHSVAQTKEQYE 236
 Qy 283 FLXHTVAQMFCTLIQ 297
 Db 237 LVHRAIAQLFEKQLQ 251

RESULT 11

US-08-685-992-16
 ; Sequence 16, Application US/08685992
 ; Patent No. 5912138
 ; GENERAL INFORMATION:
 ; APPLICANT: Tonks, Nicholas
 ; APPLICANT: Flint, Andrew J.
 ; TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 ; TITLE OF INVENTION: TYROSINE PHOSPHATASES
 ; NUMBER OF SEQUENCES: 36
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02173

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/685,992
 FILING DATE: 25-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:

FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: CSHL96-03
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-6240
 TELEFAX: 781-861-9540
 TELEX:

INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 255 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-08-685-992-16

Query Match 20.4%; Score 493.5; DB 2; Length 255;
 Best Local Similarity 43.6%; Pred. No. 5.5e-37;
 Matches 115; Conservative 36; Mismatches 94; Indels 19; Gaps 7;

Qy 47 STVAGSRPNVRRYKDVLPYDQTRVILSLLOEGHSDYINGNFRIGVDGSLAYIATQG 106
 Db 3 SQMVASASENNAKRYRNVLPYDWSRVPKPIHEEPGSDYINASFMPGLWSPQEFIATQG 62
 Qy 107 PLPHTLLDFWRLVWFEFGVKVILMACREIENGRKCEYWAQOEPLQTLGFCITLKEKW 166
 Db 63 PLPQTVGDFWRLVWQSQSHTLVMLTNCMEAGRVKCEHYWPLDSCPCTHGLRVLVGEV 122

Qy 167 LNEIDIMRLTKVTFQKESRSYVQLQYMSWPDGRGVPSPPDHMLAMVEBARR-----LQSG 221
 Db 123 MENVTVLLLLQVEEQK-TLSVRQFHYQAWPDHGVPSPPDITLAFWRMLRQWLDQTMESGP 181
 Qy 222 PEPICVHCSAGCGRTGVLCTVD-YVROLLTQMTTPDFSLFDVVLKMKRKQRPAAVQTEEQ 280
 Db 182 P---IVHCSAGVGRGTLLIALDVLRLQSQEGLGP-----FSFVRKMRERPLMVAQTEAQ 234
 Qy 281 YRELVHTVAQMFCTLIQNASPHYQ 304
 Db 235 YVFLH-----QCICGS-SNSQRPQ 253

RESULT 12

US-09-144-925-16
 ; Sequence 16, Application US/09144925
 ; Patent No. 5951979

GENERAL INFORMATION:
 APPLICANT: Tonks, Nicholas
 APPLICANT: Flint, Andrew J.
 TITLE OF INVENTION: SUBSTRATE TRAPPING PROTEIN
 TITLE OF INVENTION: TYROSINE PHOSPHATASES
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSES: HAMILTON, BROOK, SMITH & REYNOLDS, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: MA
 COUNTRY: USA
 ZIP: 02421-4799

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: Windows 95
 SOFTWARE: FastSeq for Windows Version 2.0b
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/144,925
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/685,992
 FILING DATE: July 25, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: CSHL96-03Z
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 781-861-6240
 TELEFAX: 781-861-9540
 TELEX:

INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 255 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

US-09-144-925-16

Query Match 20.4%; Score 493.5; DB 2; Length 255;
 Best Local Similarity 43.6%; Pred. No. 5.5e-37;
 Matches 115; Conservative 36; Mismatches 94; Indels 19; Gaps 7;

Qy 47 STVAGSRPNVRRYKDVLPYDQTRVILSLLOEGHSDYINGNFRIGVDGSLAYIATQG 106
 Db 3 SQMVASASENNAKRYRNVLPYDWSRVPKPIHEEPGSDYINASFMPGLWSPQEFIATQG 62
 Qy 107 PLPHTLLDFWRLVWFEFGVKVILMACREIENGRKCEYWAQOEPLQTLGFCITLKEKW 166
 Db 63 PLPQTVGDFWRLVWQSQSHTLVMLTNCMEAGRVKCEHYWPLDSCPCTHGLRVLVGEV 122
 Qy 167 LNEIDIMRLTKVTFQKESRSYVQLQYMSWPDGRGVPSPPDHMLAMVEBARR-----LQSG 221

Db 123 MENVTWLLLLQVEBQK-TLSVRQHYQAWPDHGVPSFDTLLAFWRMLRQWLQDTWEGGP 181
Qy 222 PEPICVHCSAGCGRTGVLCTVD-YVRQLLLTQMIPDPDFSLFVVLKMKRKORPAAVQTEEQ 280
Db 182 P---IVHCSAGVGTGTLIALDVLRLQLQSEGLGP-----FSFVRKWRERPLMVQTEAQ 234
Qy 281 YRFLYHTVAQMFCSSTLQNASPHYQ 304
Db 235 YVFLH-----QCICGS-SNSQPRPQ 253
RESULT 13
US-08-342-930-2
; Sequence 2, Application US/08342930
; Patent No. 5821084
; GENERAL INFORMATION:
; APPLICANT: OLMSTED, ELIZABETH A.
; APPLICANT: MAURO, LAURA J.
; APPLICANT: DAVIS, ALAN R.
; APPLICANT: DIXON, JACK E.
; TITLE OF INVENTION: OSTEOBLAST-TESTICULAR PROTEIN TYROSINE
; TITLE OF INVENTION: PHOSPHATASE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,930
; FILING DATE: 21-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KOSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: 20344-20975.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1711 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-342-930-2
Query Match 19.6%; Score 474; DB 2; Length 1711;
Best Local Similarity 39.9%; Pred. No. 5e-34;
Matches 114; Conservative 35; Mismatches 111; Indels 26; Gaps 8;
Qy 10 SELERLEARGREGAVLAGESFSDIQACSAWKADGVCSTVAGSRPENVRKRYKDLVLPYD 69
Db 1134 SFQSYEAKSAHAHQTFQFEELXEVGKQD-----PRLEASHPNITIKRYPHYLPYD 1187
Qy 70 QTRVILSLQEGHSDYINGNFIKRVGDSLAYIATQGLPHTLLDFWRLWVEFGVKVILM 129
Db 1188 HSRVRLTQLCPGPHSDYINANFIPGYSHTQEIATQGLPKLTLEDFWRLWVEQGVHILM 1247
Qy 130 ACREIENGRKRCERYAQBOEPIQTGLFCITLKE-----KWLNEDIMRLTKVTFOKER 185
Db 1248 LTVGMENGRCEHYWPANSTPVTHGHITILLAEPEDEWTRERFQLQ--HGTEQKQ-R 1304
Qy 186 SVTQLQWSPDRGVPSSPDHMLAW-----EARRLQSGSPFLCVHCSAGCGRTGLCT 241

Db 1305 RVKQLQFTTTPDHSVPEAPSSLLAFVELVQEVQATQCKG--PILVHCSAGVGRGT--- 1359
Qy 242 VDVYRQLLLTQMIPDP---FSLFVDVVLKMKRKORPAAVQTEEQVRFY 285
Db 1360 --FVALLRLRLQLEBEKVADVNTVYILRLHRLPLMIQTLTSQYIFLH 1403
RESULT 14
US-08-202-389-6
; Sequence 6, Application US/08202389
; Patent No. 5536636
; GENERAL INFORMATION:
; APPLICANT: Freeman Jr., Robert M.
; APPLICANT: Plutsky, Jorge
; APPLICANT: Neel, Benjamin G.
; APPLICANT: Rosenberg, Robert D.
; TITLE OF INVENTION: IDENTIFICATION OF NOVEL TYROSINE
; TITLE OF INVENTION: PHOSPHATASES HAVING SH2 DOMAINS
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/202,389
; FILING DATE: 28-FEB-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/983,926
; FILING DATE: 01-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/829,141
; FILING DATE: 31-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/721,112
; FILING DATE: 26-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Granahan, Patricia
; REGISTRATION NUMBER: 32,227
; REFERENCE/DOCKET NUMBER: BIH92-05WA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 595 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-202-389-6
Query Match 19.3%; Score 467; DB 1; Length 595;
Best Local Similarity 32.5%; Pred. No. 4.8e-34;
Matches 112; Conservative 57; Mismatches 109; Indels 62; Gaps 10;
Qy 22 EGAVLAG---BFSDIQACSAWKADGVCSTVAGSRPENVRKRYKDLVLPYDQTRVILSL 78
Db 237 EDTACAGWFESFIQ-----KQEVKNLHQRLEGQRPENKGRYKNILPPDHSRVL--- 289
Qy 79 QEEGH-----SDYINGNFIKRV-----DGLAYIATQGLPHTLLDFWRLWVEFGVKVI 127
Db 290 --QGSNDSNIPGSDYINANYIKNQLGPDENAKTYIASQGCLEATVDFWQMAWQENSRI 347
Qy 128 LMACEIENGKRCERYAQBOEPIQTGLFCITILKEKWLNEDIMRLTKVTFOKES--- 184

Db 348 VMTTREVCKGKNCVPMPEVGMQRAYGYPVSVTVNGEHDTE-YKLTQLQVSLDNGDLI 406
 Qy 185 RSVYQLQYMSWPDGVPSSPDHMLAMVEEARLQSGPE--PLCVHCSAGCGRTGVLCTV 242
 Db 407 REIWHYQLSWPDHGVSEPGVLSFLDQINQROESLPHAGPIIVHCSAGIGRTGTIIVI 466
 Qy 243 DYVRQLLTQMIIPDPSLFDVWLKMKRQAPAAVQTEEOYRFLYHTVAQMFCSF----- 295
 Db 467 DMLMENISTKGLDCDDIDIQTIQWRAQRSGMVQTEAQYKFIYVAIAQFIETTKKLEVL 526
 Qy 296 -----LQNA-----SPHYQNIKEN 309
 Db 527 QSQKGQSEYGNITYPPAMKNNAHAKASRTSSKHEDVYEN 566

RESULT 15
 US-08-202-389-8
 ; Sequence 8, Application US/08202389
 ; Patent No. 5536636
 ; GENERAL INFORMATION:
 ; APPLICANT: Freeman Jr., Robert M.
 ; APPLICANT: Plutsky, Jorge
 ; APPLICANT: Neel, Benjamin G.
 ; APPLICANT: Rosenberg, Robert D.
 ; TITLE OF INVENTION: IDENTIFICATION OF NOVEL TYROSINE
 ; NUMBER OF SEQUENCES: 54
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 ; STREET: Two Militia Drive
 ; CITY: Lexington
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02173
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/202,389
 ; FILING DATE: 28-FEB-1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/983,926
 ; FILING DATE: 01-DEC-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/829,141
 ; FILING DATE: 31-JAN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/721,112
 ; FILING DATE: 26-JUN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Granahan, Patricia
 ; REGISTRATION NUMBER: 32,227
 ; REFERENCE/DOCKET NUMBER: BIH92-05MA
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 861-6240
 ; TELEFAX: (617) 861-9540
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 631 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-202-389-8

Query Match 19.2%; Score 465; DB 1; Length 631;
 Best Local Similarity 30.9%; Pred. No. 8e-34;
 Matches 126; Conservative 62; Mismatches 136; Indels 84; Gaps 14;
 Qy 22 EGAVLAG---EFSDIQACSAAWKADGVCSTVAGSRPNVKNYKDVLPYDQTRVILSL 78

Db 237 EDTAKAGFWBESLQ----KQEVKNLHQRLEGORPENKGNRYKNILPPDHSRVIL--- 289
 Qy 79 QEEGH-----SDYINGNFIRGV-----DGLAVIATCGPLPHTLLDFWELVWFGVKVI 127
 Db 290 --QGRDNIPIGSDYINANYIKNQLLGPDENAKTVIAGGLEATVNDFWQMAQENSRVI 347
 Qy 128 LMACREIENGKRCERYWAQEQEPLQTLFCITLIKELKWLNEDIMLTCLKVTQKES--- 184
 Db 348 VMTTREVCKGKNCVPMPEVGMQRAYGYPVSVTVNGEHDTE-YKLTQLQVSLDNGDLI 406
 Qy 185 RSVYQLQYMSWPDGVPSSPDHMLAMVEEARLQSGPE--PLCVHCSAGCGRTGVLCTV 242
 Db 407 REIWHYQLSWPDHGVSEPGVLSFLDQINQROESLPHAGPIIVHCSAGIGRTGTIIVI 466
 Qy 243 DYVRQLLTQMIIPDPSLFDVWLKMKRQAPAAVQTEEOYRFLYHTVAQMFCSF----- 295
 Db 467 DMLMENISTKGLDCDDIDIQTIQWRAQRSGMVQTEAQYKFIYVAIAQFIETTKKLEVL 526
 Qy 296 -----LQNA-----SPHYQNIKENCAPLY-----DDALFLR 321
 Db 527 QSQKGQSEYGNITYPPAMKNNAHAKASRTSSKHEDVYEN---LHTKNKRESEEAASVR 583
 Qy 322 T-----PQALLAIPRPPGGVLRISISVPGSPGHAMADTYAEQKRGAP 363
 Db 584 QGEEQGFQEEVS-----GAVLRWPCLSPDFVEAFRDGQTHNLNLGVP 626

Search completed: August 17, 2004, 20:45:05
 Job time : 20 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:44:11 ; Search time 47 Seconds

(without alignments)
3059.120 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 2424

Sequence: 1 MSRLDSARSFLERLEARGG.....NLRIGPKGRPPPAWTRV 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2424	100.0	458	13	US-10-087-993-36
2	1754.5	72.4	453	14	US-10-243-687-7
3	1724.5	71.1	448	13	US-10-087-993-32
4	755.5	31.2	802	9	US-09-822-295-18
5	755.5	31.2	802	15	US-10-366-547-95
6	755.5	31.2	802	15	US-10-309-423-5
7	727.5	30.0	807	9	US-09-822-295-2
8	709	29.2	780	15	US-10-366-547-69
9	709	29.2	780	15	US-10-366-547-71
10	708	29.2	692	15	US-10-309-423-4
11	708	29.2	778	16	US-10-322-281-848
12	708	29.2	808	15	US-10-309-423-2
13	706	29.1	773	16	US-10-322-281-845
14	705.5	29.1	382	15	US-10-366-547-77
15	703	29.0	775	15	US-10-366-547-75

Sequence 21, Appl
Sequence 94, Appl
Sequence 94, Appl
Sequence 819, Appl
Sequence 93, Appl
Sequence 93, Appl
Sequence 6, Appl
Sequence 17, Appl
Sequence 4, Appl
Sequence 2, Appl
Sequence 8, Appl
Sequence 97, Appl
Sequence 23, Appl
Sequence 1, Appl
Sequence 87, Appl
Sequence 91, Appl
Sequence 88, Appl
Sequence 3086, Ap
Sequence 117, App
Sequence 119, App
Sequence 2, Appl
Sequence 26, Appl
Sequence 2, Appl
Sequence 14, Appl
Sequence 13, Appl
Sequence 3, Appl
Sequence 28, Appl
Sequence 30, Appl
Sequence 32, Appl
Sequence 789, App

665 27.4 312 9 US-09-788-626-21
523 21.6 235 12 US-10-087-684-94
523 21.6 235 12 US-10-218-779-94
523 21.6 235 12 US-10-072-012-819
521.5 21.5 263 12 US-10-087-684-93
521.5 21.5 263 12 US-10-218-779-93
496.5 20.5 264 14 US-10-245-539-6
493.5 20.4 313 9 US-09-788-626-17
491.5 20.3 1093 14 US-10-245-539-4
491.5 20.3 1118 14 US-10-245-539-2
491.5 20.3 1118 14 US-10-245-539-8
482.5 19.9 613 15 US-10-366-547-97
463.5 19.1 341 9 US-09-788-626-23
463 19.1 595 9 US-09-920-021A-1
463 19.1 595 15 US-10-366-547-87
463 19.1 595 15 US-10-366-547-91
463 19.1 597 15 US-10-366-547-89
463 19.1 621 15 US-10-264-049-3086
463 19.1 843 14 US-10-072-036-117
463 19.1 853 14 US-10-072-036-119
458 18.9 593 14 US-10-262-552-2
458 18.9 593 14 US-10-366-547-26
458 18.9 593 16 US-10-703-210-2
456 18.8 322 9 US-09-788-626-14
454 18.7 325 9 US-09-788-626-13
453 18.7 593 9 US-09-920-021A-3
453 18.7 593 15 US-10-366-547-28
453 18.7 593 15 US-10-366-547-30
453 18.7 593 15 US-10-366-547-32
453 18.7 593 16 US-10-444-795B-789

ALIGNMENTS

RESULT 1

US-10-087-993-36

; Sequence 36, Application US/10087993

; Publication No. US20020169303A1

; GENERAL INFORMATION:

; APPLICANT: Ullrich, Axel

; Aoki, Naohito

; Kim, Yeong Woong

; Wang, Hong Yang

; Chen, Zhengjun

; Navlor, Oliver

; Kharitonkov, Alexei Igorevich

; TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK

; AND SIRP POLYPEPTIDES AND RELATED

; PRODUCTS AND METHODS

; NUMBER OF SEQUENCES: 38

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon & Lyon

; STREET: 633 West Fifth Street

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; COMPUTER READABLE FORM:

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/087,993

; FILING DATE: 05-Mar-2002

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/877,150

; FILING DATE: June 17, 1997

; APPLICATION NUMBER: U.S. 60/019,629

FILING DATE: June 17, 1996
 APPLICATION NUMBER: U.S. 60/023,485
 FILING DATE: August 9, 1996
 APPLICATION NUMBER: U.S. 60/030,860
 FILING DATE: No. US20020169303A1ember 13, 1996
 APPLICATION NUMBER: U.S. 60/034,286
 FILING DATE: December 19, 1996
 APPLICATION NUMBER: U.S. 60/030,964
 FILING DATE: No. US20020169303A1ember 15, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 225/298
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 36:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 458 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 36:
 US-10-087-993-36

Query Match 100.0%; Score 2424; DB 13; Length 458;
 Best Local Similarity 100.0%; Pred. No. 1.8e-199;
 Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MSRLDSARGFLELRARGREGAVLAGFSDIOACSAAWKADGVCSVAGSPENVRKN 60
 Db 1 MSRLDSARGFLELRARGREGAVLAGFSDIOACSAAWKADGVCSVAGSPENVRKN 60
 Qy 61 RYKDVLPYDQTRVLSLQEGHSDYINGNFIKRGVDSLAYIATQGPLHTLLDFRLVW 120
 Db 61 RYKDVLPYDQTRVLSLQEGHSDYINGNFIKRGVDSLAYIATQGPLHTLLDFRLVW 120
 Qy 121 EFGVKVILMACREIENGKRCERYWAQEQPLQGLFCITLKEKWLNEDIMLTLLKVT 180
 Db 121 EFGVKVILMACREIENGKRCERYWAQEQPLQGLFCITLKEKWLNEDIMLTLLKVT 180
 Qy 181 QKESRSVYQLOYSWPDGVPSSPDHMLAMVEARLQGSPEPLCVHCSAGCGRTGVL 240
 Db 181 QKESRSVYQLOYSWPDGVPSSPDHMLAMVEARLQGSPEPLCVHCSAGCGRTGVL 240
 Qy 241 TVDYVROLLLTOMTPPDFSLFDVVLKMKRKPAAVQTEEQRYFLYHTVAQMFCS TLQNAS 300
 Db 241 TVDYVROLLLTOMTPPDFSLFDVVLKMKRKPAAVQTEEQRYFLYHTVAQMFCS TLQNAS 300
 Qy 301 PHYQNIKENCAPLYDDALFLRTPOALLAI PRPPGGVLRISVPGSPGHAMADTYAEQKR 360
 Db 301 PHYQNIKENCAPLYDDALFLRTPOALLAI PRPPGGVLRISVPGSPGHAMADTYAEQKR 360
 Qy 361 GAPAGAGSGTGTGTGARGAEEAPLYSKVTPRAQRGAHAEDARGTLPGRVFADQSPAG 420
 Db 361 GAPAGAGSGTGTGTGARGAEEAPLYSKVTPRAQRGAHAEDARGTLPGRVFADQSPAG 420
 Qy 421 SGAYEDVAGGAQTGGLGNFIRIGPKGPRDPPAEWTRV 458
 Db 421 SGAYEDVAGGAQTGGLGNFIRIGPKGPRDPPAEWTRV 458

RESULT 2

US-10-243-687-7
 ; Sequence 7, Application US/10243687
 ; Publication No. US20030073120A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aoki, Naohito
 ; Ullrich, Axel
 ; TITLE OF INVENTION: PROTEIN TYROSINE PHOSPHATASE PTP20
 ; AND RELATED PRODUCTS AND METHODS

NUMBER OF SEQUENCES: 7
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Fast-SEQ for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/243,687
 FILING DATE: 16-Sep-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/430,626A
 FILING DATE: 29-Oct-1999
 APPLICATION NUMBER: 08/951,260
 FILING DATE: October 16, 1997
 APPLICATION NUMBER: 60/030,860
 FILING DATE: No. US20030073120A1ember 13, 1996
 APPLICATION NUMBER: PCT/1897/00946
 FILING DATE: June 17, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 227/004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-10-243-687-7

Query Match 72.4%; Score 1754.5; DB 14; Length 453;
 Best Local Similarity 74.5%; Pred. No. 5.9e-142;
 Matches 342; Conservative 37; Mismatches 73; Indels 7; Gaps 3;
 Qy 1 MSRLDSARSFLELRARGREGAVLAGFSDIOACSAAWKADGVCSVAGSPENVRKN 60
 Db 1 MSRLDSARSFLELRARGREGAVLAGFSDIOACSAAWKADGVCSVAGSPENVRKN 60
 Qy 61 RYKDVLPYDQTRVLSLQEGHSDYINGNFIKRGVDSLAYIATQGPLHTLLDFRLVW 120
 Db 61 RYKDVLPYDQTRVLSLQEGHSDYINGNFIKRGVDSLAYIATQGPLHTLLDFRLVW 120
 Qy 121 EFGVKVILMACREIENGKRCERYWAQEQPLQGLFCITLKEKWLNEDIMLTLLKVT 180
 Db 121 EFGVKVILMACREIENGKRCERYWAQEQPLQGLFCITLKEKWLNEDIMLTLLKVT 180
 Qy 181 QKESRSVYQLOYSWPDGVPSSPDHMLAMVEARLQGSPEPLCVHCSAGCGRTGVL 240
 Db 181 QKESRSVYQLOYSWPDGVPSSPDHMLAMVEARLQGSPEPLCVHCSAGCGRTGVL 240
 Qy 241 TVDYVROLLLTOMTPPDFSLFDVVLKMKRKPAAVQTEEQRYFLYHTVAQMFCS TLQNAS 300
 Db 241 TVDYVROLLLTOMTPPDFSLFDVVLKMKRKPAAVQTEEQRYFLYHTVAQMFCS TLQNAS 300
 Qy 301 PHYQNIKENCAPLYDDALFLRTPOALLAI PRPPGGVLRISVPGSPGHAMADTYAEQKR 360
 Db 301 PHYQNIKENCAPLYDDALFLRTPOALLAI PRPPGGVLRISVPGSPGHAMADTYAEQKR 360

QY 361 GAPAGAGSGTGTGTGARGAEEAPLYSKVTPRAQREGAHAEDARGTLP-GRVPADQSPA 419
 Db 361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTEAQAQGTALGRVPADENPS 414
 QY 420 GSGAYSDVAGAGTGGGLGFLNLRIGRPKGRDPPAEWTRV 458
 Db 415 GPDAYEESVTDGAQTGGGLGFLNLRIGRPKGRDPPAEWTRV 453

RESULT 3

US-10-087-993-32
 ; Sequence 32, Application US/10087993
 ; Publication No. US20020169303A1
 ; GENERAL INFORMATION:
 APPLICANT: Ullrich, Axel
 Aoki, Naohito
 Kim, Yeong Woong
 Wang, Hong Yang
 Chen, Zhongjun
 Naylor, Oliver
 Kharitonov, Alexei Igorevich
 TITLE OF INVENTION: NOVEL PTP20, PCP-2, BDP1, CLK,
 AND SIRP POLYPEPTIDES AND RELATED
 PRODUCTS AND METHODS

NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/087,993
 FILING DATE: 05-Mar-2002
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/877,150
 FILING DATE: June 17, 1997
 APPLICATION NUMBER: U.S. 60/019,629
 FILING DATE: June 17, 1996
 APPLICATION NUMBER: U.S. 60/023,485
 FILING DATE: August 9, 1996
 APPLICATION NUMBER: U.S. 60/030,860
 FILING DATE: No. US20020169303A1ember 13, 1996
 APPLICATION NUMBER: U.S. 60/034,286
 FILING DATE: December 19, 1996
 APPLICATION NUMBER: U.S. 60/030,964
 FILING DATE: No. US20020169303A1ember 15, 1996

ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 225/298
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 453 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 SEQUENCE DESCRIPTION: SEQ ID NO: 32:

US-10-087-993-32

Query Match 71.1%; Score 1724.5; DB 13; Length 448;
 Best Local Similarity 74.2%; Pred. No. 2.2e-139;
 Matches 337; Conservative 37; Mismatches 73; Indels 7; Gaps 3;
 QY 1 MSRSLSARSFLERLEARGGREGAVLAGEFSDIQACSAAMKADGVCSTVAGSRPENVRKN 60
 Db 1 MSRQSLVRSFLEQQEARDHRKGAILAREFSDIKARSVAMKTEGVCSVKAGSQQNSKKN 60
 QY 61 RYKDVLPYDQTRVLSLLQEEGHSYINGNFIKRGVDSGLAYIATQGPLPHTLLDFWRLVW 120
 Db 61 RYKDVVPYDETFVLSLLQEEGHDYINANFIRGTDGSCAYIATQGPLPHTLLDFWRLVW 120
 QY 121 EFGVKVLMACREIENGKRCERYWAQOEPLQTLFCITLIKELWNEDIMRLTKVTF 180
 Db 121 EFGIKVILMACQETENGKRCERYWAQREPLQAGFFCITLTKETALTSITLRTLVTF 180
 QY 181 QKESRSVYQLQYMSWPDGRGVSSPDHMLAMVEEARLQSGPEPLCVHCSAGCGRTGYLC 240
 Db 181 QKESRPVHQLQYMSWPDHGVFSSSDHILTWEEARCLQGLGFLCVHCSAGCGRTGYLC 240
 QY 241 TVDYVRQLLLTQMIPPDFSLFDVILKMKQKQPAAVQTEEQYRFLYHTVAQMFCSLTQNAS 300
 Db 241 AVDYVRQLLLTQTIPPNFSLEFVLEMKQKQPAAVQTEEQYRFLYHTVAQLFSRTLQNS 300
 QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAI P3PPGGVLESISVPGSPGHAMADTYAEOKR 360
 Db 301 PLYQNLKENRAPICKDSSSLRTSALPATRSPLGVLRSISVPGPPTLPMDATYAVQKR 360
 QY 361 GAPAGAGSGTGTGTGARGAEEAPLYSKVTPRAQREGAHAEDARGTLP-GRVPADQSPA 419
 Db 361 GA-----SGS-TGPGTRAPNSTDTPIYSQVAPRIQRPVSHTEAQAQGTALGRVPADENPS 414
 QY 420 GSGAYSDVAGAGTGGGLGFLNLRIGRPKGRDPPA 453
 Db 415 GPDAYEESVTDGAQTGGGLGFLNLRIGRPKGRDPPA 448

RESULT 4

US-09-822-295-18
 ; Sequence 18, Application US/09822295
 ; Patent No. US20020119501A1
 ; GENERAL INFORMATION:
 APPLICANT: Bahija Jallal
 Gregory D. Plowman
 TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
 PTPO4 RELATED DISORDERS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq for Windows 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/822,295
 FILING DATE: 02-Apr-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/081,345
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 234/253
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 802 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-822-295-18

Query Match 31.2%; Score 755.5; DB 9; Length 802;
Best Local Similarity 44.0%; Pred. No. 9.2e-56;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;
QY 27 AGEFSDIQACSAAMKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLOEGHSDY 86
DB 25 ASEFLKLRQSTKYKADKIYPTTVAQRPNKIKKNRYKDIPLDYHSLVELSLTSDSSY 84
QY 87 INGNFIRVGDSLAYIATQGPLPHTLLDFWELVWFGVKVILMACRIENGRKRCERYA 146
DB 85 INASFIKGVGPKAYIATQGPLSTLLDFWELVWFGVKVILMACRIENGRKRCERYA 144
QY 147 QEQE-PLQTGLFCITLKEKWLNDIMRLTKVTFQKESRSVYQLOYSWMPDRGVPSSPD 205
DB 145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNEIRIYQFHYKNWPDHVPSSID 203
QY 206 HMLAMVEEARLQSGPEPLCHVCSAGCGRTGVLTVDYVRQLLLTQMIPDFSLFDVVL 265
DB 204 PIQLIWMRCYQEDDCVPCICHSAGCGRTGVICAVDYTWMLLKDGIIIPKNSFVFNLIQ 263
QY 266 KMRKORPAAVOTEQRYFLYHTVAQMFCSLTQNASPHYQNIKENCAPLYDDALFLRTPQA 325
DB 264 EMRTQPSLVQTOEQYELVSAVLELF-----KRMVDVISDNHLG-----REIQA 308
QY 326 LLATPRPPGGVLRISVPGS-----FGHAVD--TYAEQKRGAPAGAGSGTGTGTG 377
DB 309 QCSIFE-----QSLTVEADSCPLDLPKNAMRDVKTNTNHSKQGAESAESTGSSGLR 362
QY 378 ARSAEE 383
DB 363 TWNAEE 368

RESULT 5

US-10-366-547-95
Sequence 95, Application US/10366547
Publication No. US20030215899A1
GENERAL INFORMATION:
APPLICANT: Meng, Tzu-Ching
APPLICANT: Tonks, Nicholas K.
APPLICANT: Cool, Deborah E.
TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
FILE REFERENCE: 200125.439
CURRENT APPLICATION NUMBER: US/10/366,547
CURRENT FILING DATE: 2003-02-12
NUMBER OF SEQ ID NOS: 98
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 95
LENGTH: 802
TYPE: PRP
ORGANISM: Mus musculus
US-10-366-547-95

Query Match 31.2%; Score 755.5; DB 15; Length 802;
Best Local Similarity 44.0%; Pred. No. 9.2e-56;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;

QY 27 AGEFSDIQACSAAMKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLOEGHSDY 86
DB 25 ASEFLKLRQSTKYKADKIYPTTVAQRPNKIKKNRYKDIPLDYHSLVELSLTSDSSY 84
QY 87 INGNFIRVGDSLAYIATQGPLPHTLLDFWELVWFGVKVILMACRIENGRKRCERYA 146
DB 85 INASFIKGVGPKAYIATQGPLSTLLDFWELVWFGVKVILMACRIENGRKRCERYA 144
QY 147 QEQE-PLQTGLFCITLKEKWLNDIMRLTKVTFQKESRSVYQLOYSWMPDRGVPSSPD 205
DB 145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNEIRIYQFHYKNWPDHVPSSID 203
QY 206 HMLAMVEEARLQSGPEPLCHVCSAGCGRTGVLTVDYVRQLLLTQMIPDFSLFDVVL 265
DB 204 PIQLIWMRCYQEDDCVPCICHSAGCGRTGVICAVDYTWMLLKDGIIIPKNSFVFNLIQ 263
QY 266 KMRKORPAAVOTEQRYFLYHTVAQMFCSLTQNASPHYQNIKENCAPLYDDALFLRTPQA 325
DB 264 EMRTQPSLVQTOEQYELVSAVLELF-----KRMVDVISDNHLG-----REIQA 308
QY 326 LLATPRPPGGVLRISVPGS-----FGHAVD--TYAEQKRGAPAGAGSGTGTGTG 377
DB 309 QCSIFE-----QSLTVEADSCPLDLPKNAMRDVKTNTNHSKQGAESAESTGSSGLR 362
QY 378 ARSAEE 383
DB 363 TWNAEE 368

RESULT 6

US-10-309-423-5
Sequence 5, Application US/10309423
Publication No. US20040006777A1
GENERAL INFORMATION:
APPLICANT: HSC Research and Development Limited Partnership
TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases
FILE REFERENCE: 92906-2
CURRENT APPLICATION NUMBER: US/10/309,423
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/600,358
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: CA 2,220,853
PRIOR FILING DATE: 1998-01-16
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 5
LENGTH: 802
TYPE: PRP
ORGANISM: Mus musculus
US-10-309-423-5

Query Match 31.2%; Score 755.5; DB 15; Length 802;
Best Local Similarity 44.0%; Pred. No. 9.2e-56;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;

QY 27 AGEFSDIQACSAAMKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLLOEGHSDY 86
DB 25 ASEFLKLRQSTKYKADKIYPTTVAQRPNKIKKNRYKDIPLDYHSLVELSLTSDSSY 84
QY 87 INGNFIRVGDSLAYIATQGPLPHTLLDFWELVWFGVKVILMACRIENGRKRCERYA 146
DB 85 INASFIKGVGPKAYIATQGPLSTLLDFWELVWFGVKVILMACRIENGRKRCERYA 144
QY 147 QEQE-PLQTGLFCITLKEKWLNDIMRLTKVTFQKESRSVYQLOYSWMPDRGVPSSPD 205
DB 145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNEIRIYQFHYKNWPDHVPSSID 203
QY 206 HMLAMVEEARLQSGPEPLCHVCSAGCGRTGVLTVDYVRQLLLTQMIPDFSLFDVVL 265
DB 204 PIQLIWMRCYQEDDCVPCICHSAGCGRTGVICAVDYTWMLLKDGIIIPKNSFVFNLIQ 263
QY 266 KMRKORPAAVOTEQRYFLYHTVAQMFCSLTQNASPHYQNIKENCAPLYDDALFLRTPQA 325

Db 264 EMRTQPSLVQTEQYELVYSAVLELF-----KRHMVDISDNHLG-----REIQ 308
Qy 326 LLAIPRPPGGVLRISVPGS-----PGHAMAD--TYAEQKRGAPAGAGSGTGTGTG 377
Db 309 QCSIEP-----OSLTVEADSCPLDLPKAMRDVKTTHQSHKQGAESAESTGGSSGLRTS 362
Qy 378 ARSAEE 383
Db 363 TMAEE 368
RESULT 7
US-09-822-295-2
; Sequence 2, Application US/09822295
; Patent No. US20020119501A1
; GENERAL INFORMATION:
; APPLICANT: Bahija Jallal
; Gregory D. Plowman
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; PTP04 RELATED DISORDERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/822,295
; FILING DATE: 02-Apr-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/081,345
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 234/253
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 807 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-822-295-2
Query Match 30.0%; Score 727.5; DB 9; Length 807;
Best Local Similarity 46.9%; Pred. No. 2.4e-53;
Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;
Qy 27 AGEFSDIOACSAANKADGVCSTVAGSPENVRKRYKDVLPYDQTRVILSLQEGHSDY 86
Db 25 ANEFLLKRQSTKYKADTYPTTVAERPKNIKKNRYKDLPLPYDYSRVLSLITSDSDSY 84
Qy 87 INGNFIRGVDGLAYIATQGPLHTLLDFWLWVEFGVKVILMACRIENGRKRCERYWA 146
Db 85 INANFIKGVGPKYAIATQGPLSTLLDFWRLWMEYVSLIIVMACMEYMGKKRCERYWA 144
Qy 147 QEQLPQTGLFCITLIKKEKLNEDIMLRLTKVTFQKESRSVYQLQYMSWPDRCVPSPPD 205

Db 145 EPEGMQLSFGPFSVSCAEAK-RKSDYIIRTLKXFNSETRIIYQHYKNWEDHVPSSID 203
Qy 206 HMLAVNEBARRLQSGPPLCVHCSAGCGRTGLCTVDYVYRQLLLTQMIPDPFSLFDVVL 265
Db 204 PILELIWDVRCYQEDSDSVPICHCSAGCGRTGVICAIDYTWMLLXDGIPENFSVSLIR 263
Qy 266 KMRKORPAAVQTEQYRFLYHTVAQMF---CSTLQNASPHYQNIKENCAP 312
Db 264 EMRTQPSLVQTEQYELVYNAVLELFRQMDVINDKHSGETESQAKHCIP 313
RESULT 8
US-10-366-547-69
; Sequence 69, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
; APPLICANT: Meng, Tzu-Ching
; APPLICANT: Tonks, Nicholas K.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
; FILE REFERENCE: 200125.439
; CURRENT APPLICATION NUMBER: US/10/366,547
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 780
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-366-547-69
Query Match 29.2%; Score 709; DB 15; Length 780;
Best Local Similarity 41.0%; Pred. No. 8.8e-52;
Matches 144; Conservative 65; Mismatches 116; Indels 26; Gaps 7;
Qy 9 RSFLERLEA-----RGREGAVLAGEFSDIOACSAANKADGVCSTVAGSPENVRKRYK 63
Db 8 RKFQIRQVQAMKSPDHNGEDN--FARDFMLRLRLSTKYRTEKIYPTATGKEENVKXRYK 65
Qy 64 DVLPYDQTRVILSLQEGHSDYINGNFIKRGVDSGLAYIATQGPLHTLLDFWRLWVEFG 123
Db 66 DILPFDHRSVKULTKTPSQSDSYINANFIKGVYGAIVATQGPLANTVIDFWRVWWEYN 125
Qy 124 VKVILMACRIENGRKRCERYW-AQEQEPLOGLFCITLIKKEKLNEDIMLRLTKVTFQK 182
Db 126 VVIIVMACREFEMGRKRCERYWPLYGEDFITPAPFKIS-CEDEQARTDYFIRTLLEFQN 184
Qy 183 ERSRVYQLQYMSWPDRCVPSPDHMLAVNEBARRLQSGPPLCVHCSAGCGRTGLCTV 242
Db 185 ESRRLYQHYNWPDPHDVPSSFSDISLDMISLMRKYQEHEDVPICHCAGCGRTGAICAI 244
Qy 243 DYVRQLLLTQMIPDPFSLFDVVKMRKORPAAVQTEQYRFLYHTVAQMFSTLQNASPH 302
Db 245 DYTWNLLKAGTPEEFNVFNLIQEMRTQHSVAVQTKQYELVHRAIAQLFEKQLQLYEIH 304
Qy 303 YONIKENCAPLYDDALFLRTPOALLAI-----PRPGGVLRISVPG 344
Db 305 -----GAQKIADGVNEINTENNVSISIEPEKQDSPPKPPR--TRSCILVEG 347
RESULT 9
US-10-366-547-71
; Sequence 71, Application US/10366547
; Publication No. US20030215899A1
; GENERAL INFORMATION:
; APPLICANT: Meng, Tzu-Ching
; APPLICANT: Tonks, Nicholas K.
; APPLICANT: Cool, Deborah E.
; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
; FILE REFERENCE: 200125.439

; CURRENT APPLICATION NUMBER: US/10/366,547
 ; CURRENT FILING DATE: 2003-02-12
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 71
 ; LENGTH: 780
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-366-547-71

Query Match 29.2%; Score 709; DB 15; Length 780;
 Best Local Similarity 40.7%; Pred. No. 8.8e-52;
 Matches 143; Conservative 66; Mismatches 116; Indels 26; Gaps 7;
 QY 9 RSFLERLEA-----RGGREGAVLAGESDIOACSAANKADGVCSTVAGSPENVRKRYK 63
 DB 8 RKFIQRVQAMKSPDHNGEDN--FARDFMRLRLSTKYRTEKIYPTATGEKEENVKRKYK 65
 QY 64 DVLVDOTRVLISLLQBEHSDYINGNFIKGVGSLAYIATQGPLHTLDFWRLVWFEFG 123
 DB 66 DILFDSHRVKLTUTPSQSDYINANFIKGVGPKAYVATQGPLANTVIDFWRMINEYN 125
 QY 124 VKVILMACREIENGRKRCERYW-AQOEPLQTLGFCITLKEKWLNEIDIMRLTKVTFQK 182
 DB 126 VVIIVMACREFEMGRKRCERYWPLYGDPITFAFPKIS-CEDEQARTDYFIRTLLEFQN 184
 QY 183 ERSRVYQLYMSWPDGRGVSPDPHMLAMVEARLQSGPEPLCVHCSAGCGRTGLVCTV 242
 DB 185 ESRLLYQHYVWPDHDPVSPFSDILDMISLMRYQIHEHVPICIHCSAGCGRTGAICAI 244
 QY 243 DYVRQLLLTQMIPPDFSLDFVVLKQKQRPAAVQTEEQRYFLYHTVAQMFCSLQNASPH 302
 DB 245 DYTWNLLKAGKIPEEFNVNLIQEMRTQHSVQTKQYVHRAIAQLPEKQLQLYEIH 304
 QY 303 YQNKENCAPLYDDALFLRTPQALLAI-----PRPGGVLRISVPG 344
 DB 305 -----GAQKIADGVNTEINTEINMISSIEPEKQDSPPKPPR--TRSLVEG 347

RESULT 10

US-10-309-423-4
 ; Sequence 4, Application US/10309423
 ; Publication No. US20040006777A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HSC Research and Development Limited Partnership
 ; TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases
 ; FILE REFERENCE: 92906-2
 ; CURRENT APPLICATION NUMBER: US/10/309,423
 ; CURRENT FILING DATE: 2002-12-03
 ; PRIOR APPLICATION NUMBER: US/09/600,358
 ; PRIOR FILING DATE: 2000-09-25
 ; PRIOR APPLICATION NUMBER: CA 2,220,853
 ; PRIOR FILING DATE: 1998-01-16
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 4
 ; LENGTH: 692
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-309-423-4

Query Match 29.2%; Score 708; DB 15; Length 692;
 Best Local Similarity 46.7%; Pred. No. 9.1e-52;
 Matches 136; Conservative 54; Mismatches 95; Indels 6; Gaps 4;
 QY 27 AGEFSDIOACSAANKADGVCSTVAGSPENVRKRYKDVLPYDQTRVILSLQEGHSDY 86
 DB 25 ANEFLKQRQSTKYKADTKYPTTTVAENAKNKKRKYKILPYDSRVELSLTSDSSV 84
 QY 87 INGFIRKQDGLAYIATQGPLHTLDFWRLVWFEFGVKVILMACREIENGRKRCERYW 146
 DB 85 INANFIKGVGPKAYIATQGPLSTLLDFWRLWMEYSVLIIVMACMEYENGRKRCERYW 144

QY 147 QEOE-PLQTLGFCITLKEKWLNEIDIMRLTKVTFQKESRVYQLYMSWPDGRVSPSPD 205
 DB 145 EFGEMQLFEGFPFSVSCAEAK-RKSDYIIRTLKVKFNSETRTIYQFHYKXNPDHDPSSID 203
 QY 206 HMLAMVEARLQSGPEPLCVHCSAGCGRTGLVCT-VDYVRQLLLTQMIPPDFSLFDVV 264
 DB 204 PILELIDWVRVCYQEDDSVPICHCSAGCGRTGVICAIVDYTWMLLKDGIIPEFVSFLI 263
 QY 265 LMKRQKQRPAAVQTEEQRYFLYHTVAQMP---CSTLQNASPHYQNKENCAP 312
 DB 264 REMRTQREPSLVQTEQYELVYNAVLELFRQMDVIRDKHSGTESQAKHCIP 314
 RESULT 11
 US-10-322-281-848
 ; Sequence 848, Application US/10322281
 ; Publication No. US20040126762A1
 ; GENERAL INFORMATION:
 ; APPLICANT: David W. Morris
 ; APPLICANT: Marc S. Malandro
 ; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
 ; FILE REFERENCE: 529452001000
 ; CURRENT APPLICATION NUMBER: US/10/322,281
 ; CURRENT FILING DATE: 2002-12-17
 ; NUMBER OF SEQ ID NOS: 866
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 848
 ; LENGTH: 778
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-322-281-848

Query Match 29.2%; Score 708; DB 16; Length 778;
 Best Local Similarity 40.7%; Pred. No. 1.1e-51;
 Matches 143; Conservative 66; Mismatches 116; Indels 26; Gaps 7;
 QY 9 RSFLERLEA-----RGGREGAVLAGESDIOACSAANKADGVCSTVAGSPENVRKRYK 63
 DB 8 RKFIQRVQAMKSPDHNGEDN--FARDFMRLRLSTKYRTEKIYPTATGEKEENVKRKYK 65
 QY 64 DVLVDOTRVLISLLQBEHSDYINGNFIKGVGSLAYIATQGPLHTLDFWRLVWFEFG 123
 DB 66 DILFDSHRVKLTUTPSQSDYINANFIKGVGPKAYVATQGPLANTVIDFWRMINEYN 125
 QY 124 VKVILMACREIENGRKRCERYW-AQOEPLQTLGFCITLKEKWLNEIDIMRLTKVTFQK 182
 DB 126 VVIIVMACREFEMGRKRCERYWPLYGDPITFAFPKIS-CEDEQARTDYFIRTLLEFQN 184
 QY 183 ERSRVYQLYMSWPDGRGVSPDPHMLAMVEARLQSGPEPLCVHCSAGCGRTGLVCTV 242
 DB 185 ESRLLYQHYVWPDHDPVSPFSDILDMISLMRYQIHEHVPICIHCSAGCGRTGAICAI 244
 QY 243 DYVRQLLLTQMIPPDFSLDFVVLKQKQRPAAVQTEEQRYFLYHTVAQMFCSLQNASPH 302
 DB 245 DYTWNLLKAGKIPEEFNVNLIQEMRTQHSVQTKQYVHRAIAQLPEKQLQLYEIH 304
 QY 303 YQNKENCAPLYDDALFLRTPQALLAI-----PRPGGVLRISVPG 344
 DB 305 -----GAQKIADGVNTEINTEINTEINMISSIEPEKQDSPPKPPR--TRSLVEG 347

RESULT 12

US-10-309-423-2
 ; Sequence 2, Application US/10309423
 ; Publication No. US20040006777A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HSC Research and Development Limited Partnership
 ; TITLE OF INVENTION: Human Lymphoid Protein Tyrosine Phosphatases
 ; FILE REFERENCE: 92906-2
 ; CURRENT APPLICATION NUMBER: US/10/309,423
 ; CURRENT FILING DATE: 2002-12-03
 ; PRIOR APPLICATION NUMBER: US/09/600,358
 ; PRIOR FILING DATE: 2000-09-25

[illegible]

Db 126 VVIIVMACREPFGKRCRWPLYGDPITFAPFKISCENEQ-ARTDYFIRTLLEFQN 184
 QY 183 ESRVYQLQYMSWPDGRGVPSPDHMLAMVEARLQSGGPEPLCVHCSAGCGRTGVLCTV 242
 Db 185 ESRLYQHYVNWPDHDPVPSFSDILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244
 QY 243 DYVRQLLLTQMIPPDFSLFDVVLKQRKORPAAVQTEQYRFLYHTVAQMFCSLTQ 297
 Db 245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSVQTKQYELVHRAIAQLFEKQLQ 299

RESULT 15
 US-10-366-547-75
 ; Sequence 75, Application US/10366547
 ; Publication No. US20030215899A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meng, Tzu-Ching
 ; APPLICANT: Tonks, Nicholas K.
 ; APPLICANT: Cool, Deborah E.
 ; TITLE OF INVENTION: REVERSIBLE OXIDATION OF PROTEIN TYROSINE
 ; TITLE OF INVENTION: PHOSPHATASES
 ; FILE REFERENCE: 200125, 439
 ; CURRENT APPLICATION NUMBER: US/10/366,547
 ; CURRENT FILING DATE: 2003-02-12
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 75
 ; LENGTH: 775
 ; TYPE: PRT
 ; ORGANISM: Mus. musculus
 US-10-366-547-75

Query Match 29.0%; Score 703; DB 15; Length 775;
 Best Local Similarity 25.0%; Pred. No. 2.9e-51;
 Matches 194; Conservative 84; Mismatches 162; Indels 336; Gaps 17;

QY 9 RSFLERLEA-----RGREGAVLAGESDIDQASAAWKADGVCSVAGSPENVRKNRYK 63
 Db 8 RRFQIRVQAMKSPDHNGEDN--FARDFMRLRLRSTKRYTEKIYPTATGEKENVRKNRYK 65
 QY 64 DVLFPDQTRVLSLLQEGHSDYINGFIRGVDGSLAYIATQGPLHTLDFWRLVWFEFG 123
 Db 66 DILFDFHSRVKLTKTSPQSDYINAFIKGVYGPXAYVATQGFRTVIDFWRMWYFN 125
 QY 124 VKVILMACREIENGKRCERYW-AQOEPLQTLGFCITLKEKWLNEIDIMRLTKYTFQK 182
 Db 126 VVMIVMACREPFGKRCRWPLYGDPITFAPFKISCENEQ-ARTDYFIRTLLEFQN 184
 QY 183 ESRVYQLQYMSWPDGRGVPSPDHMLAMVEARLQSGGPEPLCVHCSAGCGRTGVLCTV 242
 Db 185 ESRLYQHYVNWPDHDPVPSFSDILDMISLMRKYQEHEDVPICIHCSAGCGRTGAICAI 244
 QY 243 DYVRQLLLTQMIPPDFSLFDVVLKQRKORPAAVQTEQYRFLYHTVAQMFCSLTQ----- 297
 Db 245 DYTWNLLKAGKIPEEFNVFNLIQEMRTQRHSVQTKQYELVHRAIAQLFEKQLQYIEH 304
 QY 298 -----IPRP----- 297
 Db 305 GAQKIRGNEITTTGTVSSIDSEKQSGPPKPPRTRCLVEGDAKEIILQPPHPVPTI 364
 QY 298 -----NASP----- 301
 Db 365 LTPSPPSAFTVTWQDSRYHPKPVLLHMASPEQHAPDLNRSYDKSADQWKGSESAIEH 424
 QY 302 -----HYQNIKENCAPLYDDALFLRT--PQA 325
 Db 425 IDKKLERNLSFEIKKVPLOQPKSFDGNTLLNRGHAIKIKSASSVVD-----RTSKPQE 479
 QY 326 LLA-----IPRP-----PGGVLRSI- 340
 Db 480 LSAGALKVDDVQNSCADCSAAHSHRAAESSESQNSHTPPRPDCLPLDKKGHTVWSLH 539
 QY 341 -----SVFGSPGHAMADTY-----ABEQKR----- 360

Search completed: August 17, 2004, 20:50:05
 Job time : 50 secs

Db 540 GPNATPVDPSPDGKSPDNHSQTLKTVSSSTFNSTAEAEADLTHEHNSPLLKAPLSFTN 599
 QY 361 -----GAPAGAGSGTGTGTGCA-----RSAEEAPLYSKYTPR----- 393
 Db 600 FLHSDMHSDGSGSDGAVTRNKTSISTASATVSPASSAESACHRRVLFMSIARQEVAGTP 659
 QY 394 ---AORPCGAHAEDARGTLPGRVP----- 413
 Db 660 HSGAEKADADVSEBSPPPLPEPTPESFVLADMPVPEWHELPNQEMSQRESEGLTTSGNE 719
 QY 414 -----ADQSPAGSGAYEDVA--GGAQTGGLGFNLIRGPKGPRDPPAEWT 456
 Db 720 KHDAGGIHTEASADSPAPFSDKQDQITKSPAENVTDIGFNGRCGPKGPREPPSEWT 775

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:40:39 ; Search time 17 Seconds
(without alignments)
2591.513 Million cell updates/sec

Title: US-10-087-993a-36

Perfect score: 2424
Sequence: 1 MSRLSARSFLERLEARG.....NLIRPKGRDPPEAWTRV 458

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.78.*
1: Pirl.*
2: Pirl2.*
3: Pirl3.*
4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	755.5	31.2	802	1 B44390	protein-tyrosine-p
2	710	29.3	773	1 JH0609	protein-tyrosine-p
3	709	29.2	780	1 JCL368	protein-tyrosine-p
4	705.5	29.1	382	1 S48748	protein-tyrosine-p
5	705	29.1	775	2 S55345	protein-tyrosine-p
6	491.5	20.3	1118	1 A49724	protein-tyrosine-p
7	475.5	19.6	595	1 A44390	protein-tyrosine-p
8	474	19.6	1711	1 A55148	protein-tyrosine-p
9	463	19.1	595	1 S20825	protein-tyrosine-p
10	462	19.1	926	1 A41105	protein-tyrosine-p
11	453	18.7	593	1 JN0805	protein-tyrosine-p
12	453	18.7	593	2 JC5167	protein-tyrosine-p
13	451	18.6	585	2 A46209	protein-tyrosine-p
14	449	18.5	597	1 A53593	protein-tyrosine-p
15	448	18.5	521	1 A44267	protein-tyrosine-p
16	448	18.5	913	1 A41109	protein-tyrosine-p
17	444	18.3	595	1 A55651	protein-tyrosine-p
18	442	18.2	694	2 A53978	protein-tyrosine-p
19	441	18.2	597	2 B53978	protein-tyrosine-p
20	435	17.9	1337	1 T38670	protein-tyrosine-p
21	431	17.8	398	2 T08716	protein-tyrosine-p
22	430.5	17.8	435	1 TPHUN1	protein-tyrosine-p
23	430	17.7	593	1 A42690	protein-tyrosine-p
24	429.5	17.7	583	2 S17671	protein-tyrosine-p
25	428	17.7	624	2 T19630	hypothetical prote
26	428	17.7	1026	2 T19631	protein-tyrosine-p
27	426.5	17.6	802	1 A36065	protein-tyrosine-p
28	424.5	17.5	1437	2 T31093	probable protein-t
29	424.5	17.5	2490	1 A54971	protein-tyrosine-p

30	424	17.5	1301	1 A41622	protein-tyrosine-p
31	423.5	17.5	829	1 A47373	protein-tyrosine-p
32	423	17.5	360	1 JH0692	protein-tyrosine-p
33	421.5	17.4	1238	2 S68700	Hpp beta-like tyr
34	421.5	17.4	2294	2 I67630	protein-tyrosine-p
35	421.5	17.4	2466	2 I67629	probable protein-t
36	421	17.4	1200	2 T43148	leukocyte antigen-
37	420	17.3	1898	2 S46216	receptor tyrosine
38	420	17.3	2051	2 T30938	protein-tyrosine-p
39	419.5	17.3	1188	1 A57064	protein-tyrosine-p
40	419.5	17.3	1216	2 S60613	protein-tyrosine-p
41	419.5	17.3	1997	1 S12050	protein-tyrosine-p
42	419	17.3	1442	1 B48148	protein-tyrosine-p
43	419	17.3	1445	1 A48148	protein-tyrosine-p
44	418.5	17.3	405	2 I49372	protein-tyrosine-p
45	418.5	17.3	1897	1 TDHULK	leukocyte antigen-

ALIGNMENTS

RESULT 1

B44390
protein-tyrosine-phosphatase (EC 3.1.3.48) PRP, nonreceptor type 8 - mouse
N:Alternate names: protein-tyrosine-phosphatase PEP
C:Species: Mus musculus (house mouse)
C>Date: 03-May-1994 #Sequence_revision 26-May-1994 #text_change 11-Jun-1999
C:Accession: B44390; S71952; S27876
R:Matthews, R.J.; Bowne, D.B.; Flores, E.; Thomas, M.L.
Mol. Cell. Biol. 12, 2396-2405, 1992
A:Title: Characterization of hematopoietic intracellular protein tyrosine phosphatases: c and threonine-rich sequences.
A:Reference number: A44390; MUID:92236615; PMID:1373816
A:Accession: B44390
A:Molecule type: mRNA
A:Residues: 1-802 <MAY>
A:Cross-references: GB:M90388; NID:g200522; PIDN:AAA39994.1; PID:g200523
R:Cloutier, J.F.; Veillette, A.
EMBO J. 15, 4903-4918, 1996
A:Title: Association of inhibitory tyrosine protein kinase p50(csk) with protein tyrosine phosphatase.
A:Reference number: S71952; MUID:97045099; PMID:8890164
A:Accession: S71952
A:Molecule type: mRNA
A:Residues: 495-789 <CLO>
C:Comment: This protein is found primarily in hematopoietic tissues.
C:Genetics:
C:Gene: 70zpep
C:Complex: physically associates with inhibitory tyrosine protein kinase Csk; interaction
C:Function:
A:Description: probably an effector and/or regulator of tyrosine protein kinase csk in T.
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 8; protein-tyrosine-phosphatase, phosphoric monoester hydrolase; tyrosine-specific phosphatase
C:Keywords: phosphoprotein; glutamic acid/proline/serine/threonine-rich
F:54-278/Domain: protein-tyrosine-phosphatase homology <PIP>
F:497-802/Region: glutamic acid/proline/serine/threonine-rich
F:613-621/Region: proline-rich
F:688-695/Region: proline-rich
F:227/Active site: Cys (phosphocysteine intermediate) #status predicted
F:233/Binding site: substrate phosphate (Arg) #status predicted

Query Match 31.2%; Score 755.5; DB 1; Length 802;
Best Local Similarity 44.0%; Pred. No. 2e-47;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;

QY	27	AGEPSDIOACSAWKADGVCVSRRPENKRYKDVLPYDPTRVLSLLOEGRHSDY	86
Db	25	ASEFPLKQRSTKYKADKIYFTVAQRPNKKRYKDVLPYDPTRVLSLLOEGRHSDY	84
QY	87	INGNFIRGVGDSLAYIATCGPLPHTLLDFWRLWFEVGVKVIILMACREIENGKRCERYWA	146
Db	85	INASIKGVYGFKAYIATCGPLSTLLDFWRMIWEYRILVIWVIMACNEFMGKKCERYWA	144
QY	147	QEQE-PLQTGLFCITLIIKEKWLINEDIMLTLLKVFQKESRSVYQLQYVSWPDRGVPS	205

Db 145 EPGETQLOFPFSISCAEAK-KKSDYKIRTLKAKFNNEIRIIYQFKXWPDHDPVSSID 203
 Qy 206 HMLAMTEARLQSGPEPLCVHCSAGCGRTGVLCTDYYVROLLLTQMIPPFDSLEDDVL 265
 Db 204 FILQIWMDCYQEDDCVPICHSAGCGRTGVCICAVDVTWMLLKDGIIIPKNSFVENLIQ 263
 Qy 266 KMRKORAAVQTEOYRFLVHTVAQFCSTLQNASPHYQIKENCAPLVDLALFLRTPOA 325
 Db 264 EMRTQPSLVQTEQYELVYSAVLELF-----KHMVDVSDNLHG-----REICA 308
 Qy 326 LLAIPRPFGVLRSISVPGS-----PGHAMAD--TYAEQKRGAPAGAGSGTGTGTGTG 377
 Db 309 QCSIPK-----QSLTVEADSCPLDLPKNAIRDVKTTHQSKGABAEATGGSSGLRTS 362
 Qy 378 ARSAEE 383
 Db 363 TMAEE 368

RESULT 2
 JH0609
 protein-tyrosine-phosphatase (EC 3.1.3.48) P19 - mouse
 N:Alternate names: protein-tyrosine-phosphatase PTPY43
 C:Species: Mus musculus (house mouse)
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: JH0609; PS0365; PS0366; G61180
 Biochem. Biophys. Res. Commun. 184, 1241-1249, 1992
 A:Title: Differential expression of a novel murine non-receptor protein tyrosine phosphatase
 A:Reference number: JH0609; MUID:92272714; PMID:1590786
 A:Accession: JH0609
 A:Molecule type: mRNA
 A:Residues: 1-773 <DEN>
 A:Cross-references: GB:X63440; GB:S36169; NID:G416181; PIDN:CAA45037.1; PID:G416182
 A:Experimental source: embryonic carcinoma cell, P19 cell
 A:Accession: PS0365
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 88-91, 'G', 93-110, 'G', 112-118, 'S', 120, 'T', 122 <DE2>
 A:Experimental source: embryonic carcinoma cell, P19 cell, clone PTP33
 A:Accession: PS0369
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 88-91, 'G', 93-109, 'LG', 112-120, 'T', 122 <DE3>
 A:Experimental source: embryonic carcinoma cell, P19 cell, clone PTP59
 A:Accession: PS0366
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 88-91, 'KV', 94-109, 'LA', 112-118, 'S', 120-122 <DE4>
 A:Experimental source: embryonic carcinoma cell, P19 cell, clone PTP42
 A:Y1, T.; Cleveland, J.L.; Ihle, J.N.
 Blood 78, 2222-2228, 1991
 A:Title: Identification of novel protein tyrosine phosphatases of hematopoietic cells by
 A:Reference number: A61180; MUID:92032882; PMID:1932742
 A:Accession: G61180
 A>Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 124-127, 'I', 129-229 <YIA>
 C:Comment: This protein is located in the cytoplasm.
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 12, protein-tyrosine-phosphatase
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:55-299/Domain: phosphatase catalytic domain #status predicted <PCD>
 F:58-282/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:231/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:237/Binding site: substrate phosphate (Arg) #status predicted

Query Match 29.3%; Score 710; DB 1; Length 773;
 Best Local Similarity 25.4%; Pred. No. 4.1e-44;
 Matches 195; Conservative 88; Mismatches 162; Indels 324; Gaps 20;

Qy 9 RSELERLEA-----RGREGAVLAGESFDIQACSAANKADGVCSVTAGSPPENVKRNRYK 63

Db 8 RRFQIRVOAMKSPDHNGEDN--FARDFMRLRLRSTKRTKTYPTATGEKENVKQNRK 65
 Qy 64 DVLVYDQTRVILSLQBEHSDYINGNFIRGVDSGLAYIATQGPLPHTLLDFWRLVWEFG 123
 Db 66 DILPFDHSRVKLTSTPSQSDYINANFIKGVGPKAYVATQGPFRNTVIDFWRLWIWEYN 125
 Qy 124 VKVILMACRETEGRKRCERYW-AQOEPLQTLGFCITLKEKWLNEIDIMLRILKVTFOK 182
 Db 126 VVMIVMACREPEMGRKRCERYWPLYGEDPITFAFPKISCENEQ-ARTDYFIRTLLEFQN 184
 Qy 183 ESRSVYQIQYMSWPDGRGVPSSPDHMLAMVEARLQSGPEPLCVHCSAGCGRTGVLCTV 242
 Db 185 ESRLLYQHYVWPDHVPSSFSDILNIMLMKYQEHEDVPICIHCSAGCGRTGALCAI 244
 Qy 243 DYVQLLLQIMIPDFSLFDVVLKQKQKQPAVQTEQYRFLVHTVAQMP----- 292
 Db 245 DYTWNLLKAGKIPPEFNVFLIQEMRTQRHSVQTEQYELVHRAIAQLFENSYNCMKFM 304
 Qy 293 ----- 292
 Db 305 EHRSVMYMKLPLELMSVPLIARDLSAKAAADSKLPCRRGCGQGRNTATRTSPGATHPD 364
 Qy 293 -----CSTLQNAS-----PHYQN----- 305
 Db 365 AITSFSLPNVTTCRTVTGTTQSCCTWPHOSNTQPTSTEAMINQRTNGAKSESAIBHD 424
 Qy 306 -IKENCA-----PL-----YDALFL-----RT--QALLA----- 328
 Db 425 KKLERNLSFEIKKVPLOEGPKGPFQNTLLARGHAIKIKSASSSVVDRTSKPQELSGALK 484
 Qy 329 -----IPRP-----PGVLRSI-----S 341
 Db 485 VDDVSONSCADCSAAHSHRAAESSEESQNSHTPPRDCPLDKKHVTVSLHGPENATP 544
 Qy 342 VPGSPGHAMADTY-----AEQKR----- 360
 Db 545 VPDSPDGKSPDNHSGTLTKTVSSSTPNSTAEEAHLDTSHHNSPLLKAPLSFTNPLHSDDW 604
 Qy 361 ---GAPAGAGSGTGTGTGA-----RSAAEAPLYSKVTTPR-----AQRP 397
 Db 605 HSDGSSDGAATRNKTSISTASATVSPASSAESACHRRVLPMSIARQEVAGTTPHSGAKD 664
 Qy 398 GAHAFDARGTLPGRPV----- 413
 Db 665 ADVSEESPPLPERTPESFVLADMPVRPEWHELPNQWSEQSEGLTTSQEKHDAGGI 724
 Qy 414 -----ADQSPAGSAYEDVA--GGAQTGGLGNLRIGRPKGRDPPAEWT 456
 Db 725 HTEASADSPPAFSDKXQOITKSPAETVDIGFNGCRKPKGPREPPSEWT 773

RESULT 3
 JCL1368
 protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN12, nonreceptor type 12 [validated] - human
 N:Alternate names: PTP-PEST; PTPGI
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence revision 01-Mar-1996 #text_change 21-Jun-2002
 C:Accession: JCL1368; A47506; A45496; S41746
 R:Takekawa, M.; Itoh, F.; Hinoda, Y.; Arimura, Y.; Toyota, M.; Sekiya, M.; In
 Biochem. Biophys. Res. Commun. 189, 1223-1230, 1992
 A:Title: Cloning and characterization of a human cDNA encoding a novel putative cytoplasm
 A:Reference number: JCL1368; MUID:93112015; PMID:1472029
 A:Accession: JCL1368
 A:Molecule type: mRNA
 A:Residues: 1-780 <TAK>
 A:Cross-references: DBJ:D13380; NID:G220033; PIDN:BAAC2648.1; PID:G220034
 A:Note: the authors translated the codon AGT for residue 636 as Ala
 R:Yang, Q.; Co, D.; Sommercorn, J.; Tonks, N.K.
 J. Biol. Chem. 268, 17650, 1993
 A:Reference number: A47506; MUID:93352561; PMID:8349645
 A:Accession: A47506
 A:Molecule type: mRNA

A;Title: Mutations at the murine motheaten locus are within the hematopoietic cell prote
A;Reference number: 152816; MUID:93313972; PMID:8324828
A;Accession: I65741
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 334-353, 359-382 <SHU1>
A;Cross-references: GB:963803; NID:9388449
A;Note: deletion mutation
A;Accession: I52816
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 350-358, 'EGOSPFLTTFSSLVVQVHTQ', 359-366 <SHU2>
A;Cross-references: GB:963763; NID:9388447
A;Note: insertion mutation
A;Accession: I65740
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 34-76, 'VPRPIHWAGGVTAAQOGRALD', <SHU3>
A;Cross-references: GB:963764; NID:9388450
A;Note: frameshift mutation
R;Yeung, Y.G.; Berg, X.L.; Pixley, F.J.; Angeletti, R.H.; Stanley, E.R.
J. Biol. Chem. 267, 23447-23450, 1992
A;Title: Protein tyrosine phosphatase-1C is rapidly phosphorylated in tyrosine in macroph
A;Reference number: A45143; MUID:93054686; PMID:1385421
A;Accession: A45143
A;Status: preliminary
A;Molecule type: protein
A;Residues: 137-139, 'X', 141-143, 'X', 145-151 <YE1>
A;Experimental source: BAC1.2F5 macrophage
A;Note: sequence extracted from NCBI backbone (NCBIP:118519)
A;Accession: B45143
A;Status: preliminary
A;Molecule type: protein
A;Residues: 54-56, 'X', 58, 'X', 60-61, 'X', 63-68 <YE2>
A;Experimental source: BAC1.2F5 macrophage
A;Note: sequence extracted from NCBI backbone (NCBIP:118518)
C;Comment: This protein is found primarily in hematopoietic tissues.
C;Genetics:
A;Gene: me/HCPH; motheaten
C;Function:
A;Description: catalyzes hydrolysis of peptidyl-phosphotyrosine to release phosphate
C;Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosph
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat
F;4-98/Domain: SH2 homology <SH2A>
F;110-211/Domain: SH2 homology <SH2B>
F;265-521/Domain: phosphatase catalytic domain #status predicted <PHP>
F;270-504/Domain: protein-tyrosine-phosphatase homology <PTP>
F;453/Active site: Cys (phosphocysteine intermediate) #status predicted
F;455/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.6%; Score 475.5; DB 1; Length 595;
Best Local Similarity 36.2%; Pred. No. 4.4e-27;
Matches 106; Conservative 53; Mismatches 105; Indels 29; Gaps 8;

Qy 22 EGAVLAG---EFSDIQCSAAWKADGVCSTVAGSRPENVRKNRYKDVLPDQTRVLSLL 78
Db 237 EDTAKAGFWEEFESLQ-----KQEVNLRHQLEGQRPNKKNRYKNILPFDHRSVIL--- 289
Qy 79 QEEGH-----SDYINGNFIRGV-----DGLAVIATQGLPHTLDFWLVWVFGVKVI 127
Db 290 --QGEDSNIPGSDIYNANYVKNQLLGDPSNKTIVASQGLDQVDFWQVMAQENTRVI 347
Qy 128 LMACRETENGKRCERYWAOEQLPQGLFCITILKEKWLNEDIMLRLTKVTFQKES--- 184
Db 348 VMTTREVKEGKGNKCVYMPVEGTGVVGLYSVTNSREHDTAE-YKLRLTLQISPLDNDLV 406
Qy 185 RSVYQLOVMSWPDGVPSSPDHMLAMVEARLQSGSP--PLCVHCSAGCGRTGLVCTV 242
Db 407 REIWHYQLSWPDGVPSSPDGGLVSLFDQINQROESLPHAGPIIVHCSAGIGRTIIVI 466
Qy 243 DYVQQLLTQMIPDPFSLDFVVLKMKRQPPAAVQTEBEQYRFLXHTVQAQMFCS 295
Db 467 DMLMESISTKGLDCDIDIQKTIQWVRAQRSGMWQTEAQYKFIYVAIAQFIETT 519

RESULT 8

A55148

protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type OST precursor - rat
N;Alternate names: OST-PTP; osteostecticular protein-tyrosine-phosphatase
C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A55148
R;Nauro, L.J.; Olmsted, E.A.; Skrobacz, B.M.; Mourey, R.J.; Davis, J.E.
J. Biol. Chem. 269, 30659-30667, 1994
A;Title: Identification of a hormonally regulated protein tyrosine phosphatase associated
A;Reference number: A55148; MUID:95074080; PMID:7527035
A;Accession: A55148

A;Status: not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-1711 <MAU>

A;Cross-references: GB:I36884

C;Comment: The sequence contains ten fibronectin type III repeats and two protein-tyrosin
C;Superfamily: protein-tyrosine-phosphatase, receptor type OST; fibronectin type III rep
C;Keywords: phosphoprotein; phosphoric monoester hydrolase; receptor; transmembrane prote
F;1-18/Domain: signal sequence #status predicted <SG>
F;19-1711/Product: protein-tyrosine-phosphatase, receptor type OST #status predicted <MA
F;1174-1398/Domain: protein-tyrosine-phosphatase homology <PTP1>
F;1350/Active site: Cys (phosphocysteine intermediate) #status predicted
F;1356/Binding site: substrate phosphate (Arg) #status predicted

Query Match 19.6%; Score 474; DB 1; Length 1711;

Best Local Similarity 39.9%; Pred. No. 2.2e-26;

Matches 114; Conservative 35; Mismatches 111; Indels 26; Gaps 8;

Qy 10 SFLELRAGRGREGAVLAGFSDIQCSAAWKADGVCSTVAGSRPENVRKNRYKDVLPYD 69

Db 1134 SFRQSYEAKSAHAHQTFQFEELKEVKDQ-----PRLAEHPDNIKNRYPHVLPYD 1187

Qy 70 QTRVLSLLQEEGHSDYINGNFIRVDGSLAVIATQGLPHTLDFWLVWVFGVKVILM 129

Db 1188 HSRVLTQLPGEPHSDYINANFIPGYSHTQIIATQGLPKTKLTLEDFWLVWVQQVHVIM 1247

Qy 130 ACRETENGKRCERYWAOEQLPQGLFCITILKE---KWLNEDIMLRLTKVTFQKESR 185

Db 1248 LVVGNENGLCEHWPNANSPVTHGHTIHLAEPDEWTRREFQLQ--HGTEQKQ-R 1304

Qy 186 SVYQLOVMSWPDGVPSPDHMLAMV---BEARLQSGPPEPLCVHCSAGCGRTGVCT 241

Db 1305 RVKQLQFTWPDHSPVEAFSSLLAFVQLVQEQVQATQKG--PILVHCSAGVGRGT--- 1359

Qy 242 VDVYRQLLTQMIPDP--FSLFDVVLKMKRQPPAAVQTEBEQYRELY 285

Db 1360 --FVALLRLRLQLEBEKVADVNTVYILRLHRLPLMIQTLSTQYIFLH 1403

RESULT 9

S20825

protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN6, nonreceptor type 6 [validated] - human
N;Alternate names: hematopoietic cell phosphatase HCP; protein-tyrosine-phosphatase 1C; i
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 08-Feb-1996 #text_change 21-Jun-2002
C;Accession: B42031; A38189; S20825; S17234; S20837
R;Yi, T.L.; Cleveland, J.L.; Ihle, J.N.
Mol. Cell. Biol. 12, 836-846, 1992

A;Title: Protein tyrosine phosphatase containing SH2 domains: characterization, preferen
A;Reference number: A42031; MUID:92123209; PMID:1732748
A;Accession: B42031

A;Molecule type: mRNA

A;Residues: 1-595 <Y11>

A;Cross-references: GB:M74093

A;Experimental source: T-lymphoid cell line

A;Note: sequence extracted from GenBank

R;Plutsky, J.; Neel, B.G.; Rosenberg, R.D.

Proc. Natl. Acad. Sci. U.S.A. 89, 1123-1127, 1992

A;Title: Isolation of a src homology 2-containing tyrosine phosphatase.

A;Reference number: A38189; MUID:92141214; PMID:1736296

A:Accession: A38189
 A:Molecule type: mRNA
 A:Residues: 1-85, 'V', 87-595 <PLU>
 A:Cross-references: GB:M77273; NID:g338079; PIDN:AAA36610.1; PID:g338080
 A:Note: sequence extracted from NCBI backbone (NCBIN:79619, NCBI:P:79620)
 R:Shen, S.H.; Bastien, L.; Posner, B.I.; Chretien, P.
 Nature 353, 868, 1991
 A:Title: Corrigendum: A protein-tyrosine phosphatase with sequence similarity to the SH2
 A:Reference number: S20825
 A:Accession: S20825
 A:Molecule type: mRNA
 A:Residues: 1-'LSRG', 4-595 <SH>
 A:Cross-references: EMBL:X62055; NID:g35781; PIDN:CAA43982.1; PID:g35782
 R:Shen, S.H.; Bastien, L.; Posner, B.I.; Chretien, P.
 Nature 352, 736-739, 1991
 A:Title: A protein-tyrosine phosphatase with sequence similarity to the SH2 domain of th
 A:Reference number: S17234; MUID:91343005; PMID:1652101
 A:Accession: S17234
 A:Molecule type: mRNA
 A:Residues: 1-'LSRG', 4-589, 'VPSRGSEKCPQVAMPQ' <SH2>
 A:Experimental source: breast carcinoma cells
 A:Note: sequence revised in reference S20805
 C:Genetics:
 A:Gene: GDB:PTPN6
 A:Cross-references: GDB:l31389; OMIM:176883
 A:Map position: 12p13-12p13
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosphat
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphat
 F:4-98/Domain: SH2 homology <SH2A>
 F:110-211/Domain: SH2 homology <SH2B>
 F:265-521/Domain: phosphatase catalytic domain #status predicted <P>
 F:270-504/Domain: protein-tyrosine-phosphatase homology <PT>
 F:453/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:459/Binding site: substrate phosphate (Arg) #status predicted
 Query Match 19.1%; Score 463; DB 1; Length 595;
 Best Local Similarity 32.9%; Pred. No. 3.6e-26;
 Matches 112; Conservative 56; Mismatches 110; Indels 62; Gaps 10;
 QY 22 EGAVIAG---EFSDIQACSAANKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVLSL 78
 DB 237 EDTAKAGWEEFESLQ---KQEVNLLHQRLEGQRPENKGNRYKNILPFDHSRVIL--- 289
 QY 79 QEEGH-----SDYINGNFIRGV-----DGLAYIATQGLPHTLLDFWLVWFEVGVKY 127
 DB 290 --QGRDNIQSGSDYINANYIKNQLLGDENAKTYIASQGLCATVNDPQMAWQENSRVI 347
 QY 128 LMACREIENGKRCERYWAOEQEPLQTGLFCITLKEKWLINEDIMRLTKVTFQKES--- 184
 DB 348 VMTTREVKEGKNKCVYPVWGVQRAVGPVSVINCGBHDITTE-YKLRTLQVSLDNGDLI 406
 QY 185 RSVVQLQMWPDGVPSSPDHMLAMVEEARLQGSQPE--PLCVHCSACCGTGVLCIV 242
 DB 407 REIHHYQYLSWPDHGVSEFEGVLSFLDQINQRQESLPHAGPIIVHCSAGIGSTGTIIVI 466
 QY 243 DYVRQLLLTQWIPDFSLDFVLMKVRQRPAAVQTEQVRYFLYHTVAQMFCST----- 295
 DB 467 DMLNENISTKGLDCDDIDIKTIQWVRAQRSGMVQTEAQYFIYVAQAQFIETTKKLEVL 526
 QY 296 -----LQNA-----SPHYQNIKEN 309
 DB 527 QSQKGQSEYCNITYPYPMKNNAHAKASRTSSKHKEDYEN 566
 RESULT 10
 A41105
 protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN4, nonreceptor type 4 [validated] - human
 N:Alternate names: PTPase MEG
 C:Species: Homo sapiens (man)
 C:Date: 20-Mar-1992 #sequence_revision 02-May-1994 #text_change 21-Jun-2002
 A:Accession: A41105
 R:Gu, M.; York, J.D.; Warshawsky, I.; Majerus, P.W.
 Proc. Natl. Acad. Sci. U.S.A. 88, 5867-5871, 1991
 A:Title: Identification, cloning, and expression of a cytosolic megakaryocyte protein-ty
 A:Reference number: A41105; MUID:91288564; PMID:1648233
 A:Accession: A41105
 A:Molecule type: mRNA
 A:Residues: 1-926 <GUA>
 A:Cross-references: GB:M68941; NID:g190747; PIDN:AAA36530.1; PID:g190748
 A:Experimental source: megakaryocytes, cell line MEG-10
 C:Genetics:
 A:Gene: GDB:PTPN4
 A:Cross-references: GDB:l31387; OMIM:176878
 A:Map position: 9q31-9q31
 C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 3; GLGF domain homology; p
 C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
 F:31-308/Domain: protein 4.1 membrane-binding domain homology <B41>
 F:523-597/Domain: GLGF domain homology <GLG>
 F:679-900/Domain: protein-tyrosine-phosphatase homology <PTP>
 F:852/Active site: Cys (phosphocysteine intermediate) #status predicted
 F:858/Binding site: substrate phosphate (Arg) #status predicted
 Query Match 19.1%; Score 462; DB 1; Length 926;
 Best Local Similarity 37.6%; Pred. No. 7.5e-26;
 Matches 106; Conservative 47; Mismatches 107; Indels 22; Gaps 9;
 QY 17 ARGGRGAVLAGEFSDIQACSAANKADGVCSTVAGSPENVRKNRYKDVLPYDQTRVLS 76
 DB 647 AEGITGTFLT-QFDQLYR-----KPGMTWSCA-KLPQNIKRNRYRDISPYDATRVIL- 698
 QY 77 LLQEEGSDYINGNFIRGVDSGLA---YIATQGLPHTLLDFWLVWFEVGVKILMACR 132
 DB 699 ---KGNEDYINANYINWEIPSSIIINQYIACQGLPHTCTDFQMTWEGSSMVVMLTT 754
 QY 133 EIENGRKRCERYWAOEQEPLQTGLFCITLKEKWLINEDIMRLTKVTFQK---ESRSYVOL 190
 DB 755 QVERGRVKCHQWPEPTGSSSYGCVYQVTCHEEG-NTAYIFRKMTLFNQEKESRPTQI 813
 QY 191 QYMSVPRDGVSPSPDHMLAMVEEARLQGSQPEPLCVHCSACCGTGLTCTVDYVROLLL 250
 DB 814 QYIAMPDGVDPDSSDFLDVCHVRNKRAGKEEPVHVHCSAGIGRTGLITME--TAMCL 871
 QY 251 TQMTIPPSPFLDVLKMKRQRPAAVQTEQVRYFLYHTVAQM 292
 DB 872 IECNQVYPL-DIVRTWRDORAMMIQTPSOYRFVCEAILKYI 912
 RESULT 11
 UN0805
 protein-tyrosine-phosphatase (EC 3.1.3.48) PTPN11, nonreceptor type 11 [validated] - huma
 N:Alternate names: BPTP-3; protein-tyrosine-phosphatase SHP-2; PTP1D; PTP2C; SH-PTP2; SH-
 C:Species: Homo sapiens (man)
 C:Date: 10-Mar-1994 #sequence_revision 19-May-1994 #text_change 21-Jun-2002
 C:Accession: UN0805; A46210; A47386; A47244; S27398; C44929; S31767
 R:Bastien, L.; Ranachandran, C.; Liu, S.; Adam, M.
 Biochem. Biophys. Res. Commun. 196, 124-133, 1993
 A:Title: Cloning, expression and mutational analysis of SH-PTP2, human protein-tyrosine p
 A:Reference number: UN0805; MUID:94029983; PMID:8216283
 A:Accession: UN0805
 A:Molecule type: mRNA
 A:Residues: 1-593 <BAS>
 A:Cross-references: GB:L07527; NID:g292406; PIDN:AAA17022.1; PID:g292407
 R:Voegel, W.; Lammers, R.; Huang, J.; Ullrich, A.
 Science 259, 1611-1614, 1993
 A:Title: Activation of a phosphotyrosine phosphatase by tyrosine phosphorylation.
 A:Reference number: A46210; MUID:93206095; PMID:7681217
 A:Accession: A46210
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-593 <VO>
 A:Cross-references: EMBL:X70766; NID:g35783; PIDN:CAA50045.1; PID:g35784
 A:Experimental source: SK-BR-3 mammary carcinoma cells
 A:Note: sequence extracted from NCBI backbone (NCBI:P:127775)
 R:Ahmad, S.; Banville, D.; Zhao, Z.; Fischer, E.H.; Shen, S.H.
 Proc. Natl. Acad. Sci. U.S.A. 90, 2197-2201, 1993
 A:Title: A widely expressed human protein-tyrosine phosphatase containing src homology 2

A>Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-585 <FEN>
A>Note: sequence extracted from NCBI backbone (NCBIP:127770)
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosphatase
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:6-100/Domain: SH2 homology <SH2>
F:112-214/Domain: SH2 homology <SH2>
F:273-514/Domain: protein-tyrosine-phosphatase homology <PTP>
F:463/Active site: Cys (phosphocysteine intermediate) #status predicted
F:469/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.6%; Score 451; DB 2; Length 585;
Best Local Similarity 31.0%; Pred. No. 2.7e-25;
Matches 128; Conservative 59; Mismatches 142; Indels 84; Gaps 15;

QY 1 MSRLDSARSFLERLEARGREGAVLA-----GFSDI--QACSAAMKADGVCS 47
DB 212 LKQPLNTRINAAIESR-VRELSKLAETTDKVKQGFWEFETLQOQECKLLY-----S 264

QY 48 TVAGSRPENVRNRYKDVLPYDQTRVILSLQEGH-----SDYINGNFI-----RG 94
DB 265 RKEGQRQENKNRYKNILPFDHTRVVL-----HDGDPNEPVSIVYINANIIMPEFETKCNN 320

QY 95 VDGLAYIATQGPLPHTLLDFWLVWFGVKVILMACREIENGKRCERYWAOEPLQT 154
DB 321 SKPKSVIATQGCQNTVDFWVFOENSRVITTKVEVERGSKCKVYWPDEYALKEY 380

QY 155 GLPCTILIKEKWLNEDIMRLTKVTFOKES-----RSVYQLOYSWDRGVPSPDHM 207
DB 381 GVMVRNVKES-AAHDTYTLRELKSLKVGQALLQNTERTVWQYHFTWPDHGVPSDPGV 439

QY 208 LAMVEEARLQGS--GPEPLCVHCSAGCGRTGLVCTVDYVQRLLTQMIPTDFSLFDVVL 265
DB 440 LDFLEEVHHKQESIVDAGPVVHCSAGIGRTGTFIVIDLIIIREKGVDCDIDVPTIQ 499

QY 266 KMRKQRPAAVQTEQRYFLYHTVAQMFCSLTQ-----NASPHYQNIKENCAPLYD 315
DB 500 MVRSGRQGVQTEAQYFIYNAV-QHYIETLQRIEBEQSKRKGHEYNIKSS---LVD 552

QY 316 DALFLRTPQALLAIPRPPGVLRIS 341
DB 553 GELGYTTRV-----GCPGHSVSP--MDEVDDGQWVEGLGT 585

RESULT 14
A53593
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 11 - rat
N:Alternate names: pTase L1
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A53593; S29281
R:Mei, L.; Doherty, C.A.; Haganir, R.L.
J. Biol. Chem. 269, 12254-12262, 1994
A>Title: RNA splicing regulates the activity of a SH2 domain-containing protein tyrosine
A:Reference number: A53593; MUID:94216346; PMID:7512964
A:Accession: A53593
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-597 <MEI>
A:Cross-references: GB:U05963; NID:G458332; PIDN:AAA19133.1; PID:G458333
R:Hiraga, A.; Munakata, H.; Hata, K.; Suzuki, Y.; Tsukui, S.
Eur. J. Biochem. 209, 195-206, 1992
A>Title: Purification and characterization of a rat liver protein-tyrosine phosphatase
A:Reference number: S29281; MUID:95011127; PMID:1382983
A:Accession: S29281
A:Molecule type: protein
A:Residues: 24-31;36-54;56-89;100-103;X',113-120;132-155;179-198;214-233;24
C:Superfamily: protein-tyrosine-phosphatase, nonreceptor type 6; protein-tyrosine-phosphatase
C:Keywords: alternative splicing; phosphoprotein; phosphoric monoester hydrolase; tyrosine
F:6-100/Domain: SH2 homology <SH2>
F:112-214/Domain: SH2 homology <SH2>
F:273-514/Domain: protein-tyrosine-phosphatase homology <PTP>

F:463/Active site: Cys (phosphocysteine intermediate) #status predicted
F:469/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.5%; Score 449; DB 1; Length 597;
Best Local Similarity 32.4%; Pred. No. 3.9e-25;
Matches 125; Conservative 58; Mismatches 141; Indels 62; Gaps 14;

QY 1 MSRLDSARSFLERLEARGREGAVLA-----GFSDI--QACSAAMKADGVCS 47
DB 212 LKQPLNTRINAAIESR-VRELSKLAETTDKVKQGFWEFETLQOQECKLLY-----S 264

QY 48 TVAGSRPENVRNRYKDVLPYDQTRVILSLQEGH-----SDYINGNFI-----RG 94
DB 265 RKEGQRQENKNRYKNILPFDHTRVVL-----HDGDPNEPVSIVYINANIIMPEFETKCNN 320

QY 95 VDGLAYIATQGPLPHTLLDFWLVWFGVKVILMACREIENGKRCERYWAOEPLQT 154
DB 321 SKPKSVIATQGCQNTVDFWVFOENSRVITTKVEVERGSKCKVYWPDEYALKEY 380

QY 155 GLPCTILIKEKWLNEDIMRLTKVTFOKES-----RSVYQLOYSWDRGVPSPDHM 207
DB 381 GVMVRNVKES-AAHDTYTLRELKSLKVGQALLQNTERTVWQYHFTWPDHGVPSDPGV 439

QY 208 LAMVEEARLQGS--GPEPLCVHCSAGCGRTGLVCTVDYVQRLLTQMIPTDFSLFDVVL 265
DB 440 LDFLEEVHHKQESIVDAGPVVHCSAGIGRTGTFIVIDLIIIREKGVDCDIDVPTIQ 499

QY 266 KMRKQRPAAVQTEQRYFLYHTVAQMFCSLTQ-----NASPHYQNIKENCAPLYD 315
DB 500 MVRSGRQGVQTEAQYFIYNAV-QHYIETLQRIEBEQSKRKGHEYNIKSS---LVD 555

QY 316 DALFLRTPQALLAIPRPPGVLRIS 341
DB 556 QTSQDSPLP-PCPTPTPPCAEMREDS 580

RESULT 15
A44267
protein-tyrosine-phosphatase (EC 3.1.3.48), nonreceptor type 1 - slime mold (Dictyostelium
C:Species: Dictyostelium discoideum
C>Date: 30-Apr-1993 #sequence_revision 08-Mar-1996 #text_change 24-Apr-1998
C:Accession: A44267
R:Howard, P.K.; Sefton, B.M.; Firtel, R.A.
Cell 71, 637-647, 1992
A>Title: Analysis of a spatially regulated phosphotyrosine phosphatase identifies tyrosin
A:Reference number: A44267; MUID:93046662; PMID:1423620
A:Accession: A44267
A>Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA; DNA
A:Residues: 1-521 <HOW>
A>Note: sequence extracted from NCBI backbone (NCBIP:117713)
C:Superfamily: Dictyostelium protein-tyrosine-phosphatase, nonreceptor type 1; protein-ty
C:Keywords: phosphoprotein; phosphoric monoester hydrolase; tyrosine-specific phosphatase
F:121-459/Domain: protein-tyrosine-phosphatase homology #status atypical <PTP>
F:310/Active site: Cys (phosphocysteine intermediate) #status predicted
F:316/Binding site: substrate phosphate (Arg) #status predicted

Query Match 18.5%; Score 448; DB 1; Length 521;
Best Local Similarity 29.0%; Pred. No. 3.9e-25;
Matches 113; Conservative 53; Mismatches 88; Indels 136; Gaps 13;

QY 44 GVCSTVAGSRPENVRNRYKDVLPYDQTRVILSLQEGHSDYINGNFIIRGVDSGL--AY 101
DB 109 CPSETSEGDKEENTSKRYTNILPVNTRVQLKIQKESDYINANYI---DGAYPKQF 165

QY 102 IATQGPLPHTLLDFWLVWFGVKVILMACREIENGKRCERYWAOEPLQTGLF---- 157
DB 166 ICTQGPLNTIADFRWVWENRCRIIVMLSRESENCRICKDRYWPQIGQEQSIIYNGN 225

QY 158 -----CITLLIKKWLNEDIMRLTKVTFOKESRSVYQLOYSWDRGVPSPDH-- 206
DB 226 EVFGTYSVELVEVQLDP--EKEITNIRLITFEGETDITQYQEGWPDHNI---PDHTQ 280

Qy	207	-----MLAMVEEARLQSGPE--PLCVHCSAGCGRTGVLCTV-----DYVROLLT	251
Db	281	PFQQLHSITNRQNIIFSSDRNVPIIVHCSAGVGTGTECTAVIMMKLDHYFKOLDAT	340
Qy	252	---QMIPP-----	256
Db	341	PIDQVDPFTHLPITEYQSDNLDLGLGYHFKSSIYNSNGINNNNNNNNNNNNNNNNN	400
Qy	257	-----DFSLEFVVVKMRKORPAAVQTEEQY	281
Db	401	GSNNTPQTEPNNEEDDDAAESTKYAIDMKYNSRIDENLFSIVLKLREQRFQGMVQLEQY	460
Qy	282	REFLYHTV-AQMF-----CSTLQNASPHYCNI	306
Db	461	LFCYKTLAEIYHRLNCK-LGFSLPHVNNI	489

Search completed: August 17, 2004, 20:44:35
Job time : 18 secs

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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:29:38 ; Search time 14 Seconds
(without alignments)
1703.438 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 2424

Sequence: 1 MSRLDSARSFLERARGG.....NLRIKRGKPRDPPAEWTRV 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2424	100.0	458	1 PTNI_HUMAN	Q99952 homo sapien
2	755.5	31.2	802	1 PTNB_MOUSE	P29352 mus musculu
3	727.5	30.0	807	1 PTNB_HUMAN	Q9Y2R2 homo sapien
4	709	29.2	780	1 PTNC_HUMAN	Q05209 homo sapien
5	703	29.0	775	1 PTNC_MOUSE	P35831 mus musculu
6	485	20.0	1705	1 PTPV_MOUSE	P70289 mus musculu
7	482.5	19.9	613	1 PTN6_RAT	P81718 rattus norv
8	475.5	19.6	595	1 PTN6_MOUSE	P29351 mus musculu
9	474	19.6	1711	1 PTPV_RAT	Q64612 rattus norv
10	463	19.1	595	1 PTN6_HUMAN	P29350 homo sapien
11	462	19.1	926	1 PTN4_HUMAN	P29074 homo sapien
12	453	18.7	593	1 PTNB_CHICK	Q90687 gallus gall
13	453	18.7	593	1 PTNB_HUMAN	Q06124 homo sapien
14	451	18.6	585	1 PTNB_MOUSE	P35235 mus musculu
15	448	18.5	593	1 PTNB_RAT	P41499 rattus norv
16	448	18.5	913	1 PTN3_HUMAN	P36045 homo sapien
17	447	18.4	521	1 PTP1_DICDI	P34137 dictyosteli
18	435	17.9	1337	1 PTPJ_HUMAN	Q12913 homo sapien
19	430.5	17.8	435	1 PTN1_HUMAN	P18031 homo sapien
20	430	17.7	593	1 PTN9_HUMAN	P43378 homo sapien
21	428	17.7	1026	1 PTP1_CAEEL	P28191 caenorhabdi
22	426.5	17.6	802	1 PTPA_HUMAN	P18433 homo sapien
23	426	17.6	434	1 PTN1_CHICK	Q13016 gallus gall
24	424	17.5	1301	1 PTP9_DROME	P35832 drosophila
25	423.5	17.5	829	1 PTNA_MOUSE	P18052 mus musculu
26	421.5	17.4	1238	1 PTPJ_MOUSE	Q64455 mus musculu
27	421.5	17.4	2316	1 PTPZ_RAT	Q62656 rattus norv
28	421.5	17.4	2485	1 PTND_HUMAN	Q12923 homo sapien
29	420	17.3	360	1 PTN7_HUMAN	P35236 homo sapien
30	419.5	17.3	1216	1 PTPO_HUMAN	Q16827 homo sapien
31	419.5	17.3	1997	1 PTPB_HUMAN	P23467 homo sapien
32	419	17.3	1442	1 PTPG_MOUSE	Q05909 mus musculu
33	419	17.3	1445	1 PTPG_HUMAN	P23470 homo sapien

34	418.5	17.3	1897	1 PTPF_HUMAN	P10586 homo sapien
35	417.5	17.2	1912	1 PTPD_HUMAN	P23468 homo sapien
36	417	17.2	2200	1 LAR_CAEEL	Q9bmn8 caenorhabdi
37	416	17.2	1454	1 PTPT_MOUSE	Q99m80 mus musculu
38	416	17.2	1463	1 PTPT_HUMAN	O14522 homo sapien
39	415.5	17.1	1462	1 PTPM_MOUSE	P28828 mus musculu
40	414.5	17.1	359	1 PTN7_RAT	P49445 rattus norv
41	414.5	17.1	1015	1 PTPX_HUMAN	Q92932 homo sapien
42	413.5	17.1	1948	1 PTNS_HUMAN	Q13332 homo sapien
43	413.5	17.1	2314	1 PTPZ_HUMAN	P23471 homo sapien
44	412.5	17.0	1013	1 PTPX_MACNE	O02695 macaca neme
45	411.5	17.0	432	1 PTN1_RAT	P20417 rattus norv

ALIGNMENTS

RESULT 1

ID	PTNI_HUMAN	STANDARD;	PRT;	458 AA.
AC	Q99952;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Protein-tyrosine phosphatase, non-receptor type 18 (EC 3.1.3.48)			
DE	(brain-derived phosphatase).			
GN	PTPN18 OR BDPI.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND CHARACTERIZATION.			
RC	TISSUE=Brain;			
RX	MEDLINE=97108674; PubMed=8950995;			
RA	Kim Y.W., Wang H.Y., Suess I., Lambers R., Martell K.J., Ullrich A.;			
RT	"Characterization of the PEST family protein tyrosine phosphatase			
RT	BDPI.";			
RL	Oncogene 13:2275-2279(1996).			
CC	-I- FUNCTION: Differentially dephosphorylate autophosphorylated			
CC	tyrosine kinases which are known to be overexpressed in tumor			
CC	tissues.			
CC	-I- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein			
CC	tyrosine + phosphate.			
CC	-I- TISSUE SPECIFICITY: Expressed in brain, colon and several tumor-			
CC	derived cell lines.			
CC	-I- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.			
CC	Non-receptor class subfamily.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; X79568; CAA56105.1; -			
DR	HSSP; Q06124; 2SHP; PTPN18.			
DR	Genew; HGNC:9649; PTPN18.			
DR	MIM; 606587; -			
DR	GO; GO:0004726; F:non-membrane spanning protein tyrosine phos. . .; TAS.			
DR	GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.			
DR	InterPro; IPR000387; TYR_phosphatase.			
DR	InterPro; IPR000242; Tyr_PP			
DR	Pham; PF00102; Y_phosphatase; 1.			
DR	PRINTS; PR00700; ERTYPHPTASE.			
DR	SMART; SM00194; PTPC; 1.			
DR	PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.			
DR	PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.			
DR	PROSITE; PS50055; TYR_PHOSPHATASE_PTP; 1.			
KW	Hydrolase.			
FT	DOMAIN 26 291 PROTEIN-TYROSINE PHOSPHATASE.			

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FT ACT_SITE 229 229 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY)
SQ SEQUENCE 458 AA; 50384 MW; 46BCA1E17C2C78B1 CRC64;

Query Match 100.0%; Score 2424; DB 1; Length 458;
Best Local Similarity 100.0%; Pred. No. 1.7e-160;
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRLDSARSFLERLEARGREGAVLAGEFSDIQAQSAAMKADGVCSTVAGSRPENVRKN 60
DQ 1 MSRLDSARSFLERLEARGREGAVLAGEFSDIQAQSAAMKADGVCSTVAGSRPENVRKN 60
QY 61 RYKQVLPYDQTRVLSLLOEGHSDYINGNPIRGVDSGLAYIATQGPLPHTLLDFWELVW 120
DQ 61 RYKQVLPYDQTRVLSLLOEGHSDYINGNPIRGVDSGLAYIATQGPLPHTLLDFWELVW 120
QY 121 EFGVKVILMACREIENGRKCRERYWAQOEPLQGLFCITILKEKWLNEIMLRLTKVTF 180
DQ 121 EFGVKVILMACREIENGRKCRERYWAQOEPLQGLFCITILKEKWLNEIMLRLTKVTF 180
QY 181 QKESRSVYQLYNGWPDGVPSSPDHMLAMVEEARLQGSGLPEPLCHVCSAGCGRTGVL 240
DQ 181 QKESRSVYQLYNGWPDGVPSSPDHMLAMVEEARLQGSGLPEPLCHVCSAGCGRTGVL 240
QY 241 TVDYVQRLQLTQMTIPDPFSLFDVVLKMKRKPAAVQTEEOYRFLYHTVAQMFCTILQNAS 300
DQ 241 TVDYVQRLQLTQMTIPDPFSLFDVVLKMKRKPAAVQTEEOYRFLYHTVAQMFCTILQNAS 300
QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLSISVPGSPGHAMADTYAEQKR 360
DQ 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPPGGVLSISVPGSPGHAMADTYAEQKR 360
QY 361 GAPAGAGSGTGTGTGARSAREAPLYSKVTTPRAORGAHAEDARGTLGRVADOSPAG 420
DQ 361 GAPAGAGSGTGTGTGARSAREAPLYSKVTTPRAORGAHAEDARGTLGRVADOSPAG 420
QY 421 SGAYEDVAGGAQTGLGFNLRIKRPKPRPPPAETWTRV 458
DQ 421 SGAYEDVAGGAQTGLGFNLRIKRPKPRPPPAETWTRV 458

RESULT 2
PTN8 MOUSE STANDARD; PRT; 802 AA.
AC P29352;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 8 (EC 3.1.3.48)
DE (Hematopoietic cell protein-tyrosine phosphatase 702-PEP).
GN PTN8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=92236615; PubMed=1373816;
RA Matthews R.J., Bowne D.B., Flores E., Thomas M.L.;
RT "Characterization of hematopoietic intracellular protein tyrosine
RT phosphatases: description of a phosphatase containing an SH2 domain
RT and another enriched in proline-, glutamic acid-, serine-, and
RT threonine-rich sequences."
RL Mol. Cell. Biol. 12:2396-2405(1992).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Spleen, thymus, lymph node and bone marrow.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
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CC -----
CC EMBL; M90388; AAA39994.1; -.
CC PIR; B44390; B44390.
CC PDB; 1JEG; 31-OCT-01.
CC MGI; MGI:107170; Ptpn8.
CC InterPro; IPR000387; TYR phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00700; PRTPHPTASE.
CC SMART; SM00194; PTPC; 1.
CC PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
CC PROSITE; PS00056; TYR PHOSPHATASE 2; 1.
CC PROSITE; PS00055; TYR PHOSPHATASE_PTP; 1.
CC Hydrolase; 3D-structure.
CC KW DOMAIN 23 288 PROTEIN-TYROSINE PHOSPHATASE. (BY
CC FT ACT_SITE 227 227 PHOSPHOCYSTEINE INTERMEDIATE
CC SIMILARITY)
CC SQ SEQUENCE 802 AA; 89714 MW; 0F1E45339D4613E CRC64;

Query Match 31.2%; Score 755.5; DB 1; Length 802;
Best Local Similarity 44.0%; Pred. No. 8.2e-45;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;

QY 27 AGEFSDIQAQSAAMKADGVCSTVAGSRPENVRKNRYKQVLPYDQTRVLSLLOEGHSDY 86
DQ 25 ASEFLKXQSTKYKADKIYPTTVAQRPNKIKKRYKQVLPYDQTRVLSLLOEGHSDY 84
QY 87 INGNIRGVDSGLAYIATQGPLPHTLLDFWELVWFGVKVILMACREIENGRKCRERYWA 146
DQ 85 INASIRGVGPKAYIATQGPLSTLLDFWELVWFGVKVILMACREIENGRKCRERYWA 144
QY 147 QSQE--PLQTGLFCITILKEKWLNEIMLRLTKVTFQKESRSVYQLYNGWPDGVPSSPD 205
DQ 145 EPGETQLQFGPFSISCEAEK-KKSDYKIRTLKAKFNNETRIIYQHYKQWPDHVPSSID 203
QY 206 EMLAMVEEARLQGSGLPEPLCHVCSAGCGRTGVLCTVDYVQRLQLTQMTIPDPFSLFDVVL 265
DQ 204 PIQLIWDRCYQEDDCVPICIHCSAGCGRTGVICADVYTWMLLKDGIIIPKQFVFNLIQ 263
QY 266 KMKRKPAAVQTEEOYRFLYHTVAQMFCTILQNASPHYQNIKENCAPLYDDALFLRTPQA 325
DQ 264 EMRTQRPVSLVOTQRYELVYSAVLELF-----KRWMDVISDNHLG-----RIQA 308
QY 326 LLAIPTPPGGVLSISVPGS-----PGHAMAD--TYAEQKRGAPAGAGSGTGTGTG 377
DQ 309 QCSIPD-----QSILTEADSCPLDLPKAMRDVKTNTNQHSKQGAEESTGSSGLR 362
QY 378 ARSABE 383
DQ 363 TNNABE 368

RESULT 3
PTN8 HUMAN STANDARD; PRT; 807 AA.
AC Q9VZK2; O95063; O95064;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 22 (EC 3.1.3.48)
DE (Hematopoietic cell protein-tyrosine phosphatase 702-PEP) (Lymphoid
DE phosphatase) (Lyp?).
CC PTN22 OR PTPN8.
CC Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP RX SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND CHARACTERIZATION.
RA MEDLINE=9916989; PubMed=10068674;
RA Cohen S., Dadi H., Shaoul E., Sharfe N., Roifman C.M.;
RT "Cloning and characterization of a lymphoid-specific, inducible human
RL protein tyrosine phosphatase, Lyp.";
RN Blood 93:2013-2024(1999).
[2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RA Liu T., Zhang J., Fu G., Zhang Q., Ye M., Zhou J., Wu J., Shen Y.,
RA Yu M., Chen S., Mao M., Chen Z.;
RT "Human protein tyrosine phosphatase (702pep) homolog.";
RL submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Seems to act on Cbl. May play a role in regulating the
CC function of Cbl and its associated protein kinases.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Lyp1;
CC IsoId=Q9Y2R2-1; Sequence=Displayed;
CC Name=2; Synonyms=Lyp2;
CC IsoId=Q9Y2R2-2; Sequence=VSP_005134;
CC -!- TISSUE SPECIFICITY: Predominantly expressed in lymphoid tissues
CC and cells. Isoform 1 is expressed in thymocytes and both mature B
CC and T cells.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
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CC -----
DR EMBL; AF001846; AAD0904.1; -
DR EMBL; AF001847; AAD0905.1; -
DR EMBL; AF077031; AAD27764.1; -
DR HSSP; P29350; 1GWZ.
DR Genew; HGNC:9652; PTPN22.
DR MIM; 600716; -
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_Pp.
DR Pfam; PF00102; Y phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS50055; TYR_PHOSPHATASE_Ptp; 1.
KW Hydroxylase; Alternative splicing.
FT DOMAIN 23 288 PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 227 227 PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT VARSPPLIC 685 807 ELHODRSSPPPLPPTERTLESFFLADEDCMOAQIETVSTSY
FT PDWENSTSSKQTLTKPKSFTSKSLKILRNKKKICNSC
FT PPNKPAESVQSNSSSFLNFGFANRFSKPGKPNPPTWNI
FT -> GNKFSWL (in isoform 2).
FT -> FTID=VSP_005134.
FT KP -> NA (IN REF. 1).
FT V -> G (IN REF. 2).
FT G -> V (IN REF. 2).
FT I -> IV (IN REF. 1).
FT L -> P (IN REF. 2).
FT S -> W (IN REF. 2).
FT P -> S (IN REF. 2).
SQ SEQUENCE 807 AA; 91704 MW; 1ABE8AE89C9D9FBF CRC64;
Query Match 30.0%; Score 727.5; DB 1; Length 807;
Best Local Similarity 46.9%; Pred. No. 7.1e-43;
Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;
```

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QY 27 AGEFSDIQACSAAMKADGVCSTVAGSRPENVRKNRYKDVLPYDQTRVILSLQEEGHSY 86
DB 25 ANEFLKLRQSTKYKADKTYPTTVAEKPKNKRYKDLFPDYSRVLSLTSDESSY 84
QY 87 INGNFIRGVDGSLAVIATCGPLPHTLLDFWLVWFEFGVKVILMACREIENGKRCERYA 146
DB 85 INANFIKGYIGPKAYIATCGPLSTLLDFWRMIWEYSVLLIIVMACMEYENGKKCERYA 144
QY 147 QOQF-PLOTGLFCITLIKEKWLNEIMLRTLKVTFOKESRSVYQLQYQSWPDRGVPSPPD 205
DB 145 EFGENQLEFGFSPVSCAEK-RKSDYIIRTLKVENSETRIYQHYKNWPDHDPSSID 203
QY 206 HMLAMVEBARRLQSGPPEPLCVHCSAGCGRTGVLCTVDYVROLLTQIMPDPFSFDVVL 265
DB 204 PILELIMDVRCYQEDDSVPICIHCSAGCGRTGVCIDAYTWMLLKDGIIPEPVSFSLIR 263
QY 266 KVRKORPAAVOTEQRYLYHTVAQWF---CSTLQNASPHYQNIKENCAP 312
DB 264 EXRTQPSLVQEQEYELVNAVLELFRQMDVIRKDHSGTESQAHGCIIP 313
RESULT 4
PTNC HUMAN STANDARD; PRT; 780 AA.
ID PTNC HUMAN Q05209; Q16130;
AC DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 12 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase G1) (PTPG1).
GN PTPN12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=93112015; PubMed=1472029;
RA Takekawa M., Itoh F., Hinoda Y., Arimura Y., Toyota M., Sekiya M.,
RA Adachi M., Imai K., Yachi A.;
RT "Cloning and characterization of a human cDNA encoding a novel
RT putative cytoplasmic protein-tyrosine-phosphatase.";
RL Biochem. Biophys. Res. Commun. 189:1223-1230(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93203262; PubMed=8454633;
RA Yang Q.C., Tonks N.K., Sommercorn J.;
RT "Cloning and expression of PTP-PEST. A novel, human, nontransmembrane
RT protein tyrosine phosphatase.";
RL J. Biol. Chem. 268:6622-6628(1993).
RN [3]
RP SEQUENCE OF 59-136 FROM N.A., AND VARIANT COLON CANCER ARG-61.
RX MEDLINE=94156037; PubMed=7509295;
RA Takekawa M., Itoh F., Hinoda Y., Adachi M., Ariyama T., Inazawa J.,
RA Imai K., Yachi A.;
RT "Chromosomal localization of the protein tyrosine phosphatase G1 gene
RT and characterization of the aberrant transcripts in human colon
RT cancer cells.";
RL FEBS Lett. 339:222-228(1994).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- DISEASES: DEFECTS IN PTPN12 ARE FOUND IN SOME COLON CANCERS.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -----
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CC CC -----
CC EMBL: D13380; BAA02648.1; -
CC DR EMBL: M93425; AAB36529.1; -
CC DR EMBL: S69184; AAB30047.2; -
CC DR PIR: JCI368; JCI368.
CC DR HSSP: Q06124; 2SHP.
CC DR Genew: HGNC:9645; PTPN12.
CC DR MIN: 600079; -.
CC DR GO: GO:0005737; C:cytoplasm; TAS.
CC DR GO: GO:0005625; C:soluble fraction; TAS.
CC DR GO: GO:0004726; F:non-membrane spanning protein tyrosine phosphatase; TAS.
CC DR GO: GO:0006470; P:protein amino acid dephosphorylation; TAS.
CC DR InterPro: IPR000387; TYR_P.
CC DR Pfam: PF00102; Y_phosphatase; 1.
CC DR PRINTS: PR00700; PRTYPHPTASE.
CC DR SMART: SM00194; PTPc; 1.
CC DR PROSITE: PS00383; TYR_PHOSPHATASE_1; 1.
CC DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.
CC DR PROSITE: PS00055; TYR_PHOSPHATASE_PTP; 1.
CC DR Hydrolase: Disease mutation.
CC FT DOMAIN 27 291 PROTEIN-TYROSINE PHOSPHATASE.
CC FT ACT_SITE 231 231 SIMILARITY.
CC FT VARIANT 61 61 K->R (in colon cancer).
CC FT CONFLICT 121 121 V->I (IN REF. 2).
CC FT CONFLICT 322 322 V->I (IN REF. 2).
CC FT SEQUENCE 780 AA; 88092 MW; 48F7BE5FDA8F7512 CRC64;

Query Match 29.28; Score 709; DB 1; Length 780;
Best Local Similarity 41.08; Pred. No. 1.3e-41;
Matches 144; Conservative 65; Mismatches 116; Indels 26; Gaps 7;

QY 9 RSFLERLEA-----RGGREGAVLAGFSDIQACSAAMKADGVSTVAGSRPENVRKRYK 63
DB 8 RKFTQVQAMKSPDHNGEDN--FARDFMRLRLSTKYRTEKIYPTATGEEKENVKRKYK 65

QY 64 DVLFDYDQTRVLSLQBECHSDYINGFIRGVDGSLAYIATQGPLHTLLDFWLVWVEFG 123
DB 66 DILFDFHSRVKLTUKTSPQSDSYINANFIRGVGPKAYATQGPLANTVIDFWRMWEYN 125

QY 124 VKVTLMACREIENGKRCERYW-AQOEPLQDTGLFCITLKEKWLNEDIMRLTKVTFQK 182
DB 126 VVLIIVMACREFENGKRCERYWPLYGDDPTTFAPKIS-CEDSQARTDYFIRLLLEFQN 184

QY 183 ESRVYQLQNSWPDGVPSPDRMLAMVEARLQSGPEPLCVHCSACGRTGLCTV 242
DB 185 ESRRLYQHYVWPDHDPVSPSFDLSIDMLIRMKYQBEHDVFCIHCACGRTGAICAI 244

QY 243 DYVRLQLLTQMI PPDFSLFDVLKWRQRPAAVQTEQYRFLVHTVAQMFCSLTQNASPH 302
DB 245 DYTWNLLKAGKIPPEFVFNLIQEMRTQRHSVAQTKEQYELVHRAQLPEKQLQYEH 304

QY 303 YQNIKENCAPLYDALLFRTQALLAI-----PRPGGVLRISVPG 344
DB 305 -----GAQKIADGVNENINENMVSVIEPEKQSDPPPKPR--TRSLVEG 347

RESULT 5
PTNC MOUSE STANDARD; PRT; 775 AA.
AC P35831;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE (Protein-tyrosine phosphatase, non-receptor type 12 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase P19) (P19-PTP) (MPTP-PEST).
GN PTPN12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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FT CARBOHYD 982 982 N-LINKED (GLCNAC... (POTENTIAL).
SQ SEQUENCE 1705 AA; 186795 MW; 2783755F15387D5B CRC64;
Query Match 20.0%; Score 485; DB 1; Length 1705;
Best Local Similarity 33.4%; Pred. No. 1e-25;
Matches 134; Conservative 52; Mismatches 163; Indels 52; Gaps 12;
QY 8 ARSFLELEARGGREGAVLAGESDIOACSAANKADGVCSTVAGSRPENVRKRYKDVLP 67
DB 1132 SHSPRQYEAASAPAHQAFQEHFELKEVKDQ-----PRLEAEPANITKRYHVL 1185
QY 68 YDQTRVILSLQEBHSDYINGNFIQVDSGLAYIATQGLPHITLLDFWRLWVEFGVKY 127
DB 1186 YDSRVELTQSGPHSDYINANFIPGYPHQBIATQGLPKKTVDFWRLWVEQGVHVI 1245
QY 128 LMACREIENGKRCERYWAQEQPLQGLFCITLKE---KWLNEIDIMLRTLVTFQKE 183
DB 1246 IMLTVGMENGRCVLCHEHVPVNSTPVTGHITTHLLAESEDEWTRREFQLOH---GAEOK 1302
QY 184 SRSYVQLQYMSWPRGVPSSPDHMLMV---BEARLQSGPEPLCVHCSAGCGRTGV- 238
DB 1303 QRRYKQLQFTWPDHSPVPSSLLAFVELVQEVKATQKG--PILVHCSAGVGRITGF 1360
QY 239 LCTVDYVROLLLTQMIIPDPSLFDVVLKQKQRAAVQTEQRYFLYHTVAQFCTLQN 298
DB 1361 VALLPAVRQLEEEQV---DVNTVYILRLHPLMTQLSQYIFLHSLCLNKILSGPSD 1416
QY 299 ASHP----YQNIKENCA--PLYDDALFLRTPOAL-LAIAPPPGGVLSRISVPGSPGHAMA 351
DB 1417 ASDSGPVPVNFPAQACAKRANANAGFLKRYLLKQAIKDETGLSLES---PDYNQNSIA 1473
QY 352 DTYAEOK-----RGAPAGAGSGTQGT 374
DB 1474 SCHRSQQLALVEESPADNMLAASLPFGPGSGRHHVVLTS 1514
RESULT 7
PTN6_RAT STANDARD; PRT; 613 AA.
AC P81718;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE (Protein-tyrosine phosphatase, non-receptor type 6 (EC 3.1.3.48))
DE (Protein-tyrosine phosphatase SHP-1).
GN PTPN6.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
FA Aoki N., Yamaguchi Aoki Y., Ullrich A.;
RT "The rat SH2-containing protein-tyrosine phosphatase SHP-1 is a
RT positive regulator of NGF-induced neuronal differentiation of PC12
RT cells.";
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Plays a key role in hematopoiesis. This PTPase activity
CC may directly link growth factor receptors and other signaling
CC proteins through protein-tyrosine phosphorylation. The SH2 regions
CC may interact with other cellular components to modulate its own
CC phosphatase activity against interacting substrates (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBUNIT: Monomer (By similarity). Binds PTPNS1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -!- SIMILARITY: Contains 2 SH2 domains.
CC
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CC
CC EMBL; U77038; AAD00262.1; -;
CC HSSP; P29350; 1GKZ.
CC InterPro; IPR000980; SH2.
CC InterPro; IPR000387; TYR_phosphatase.
CC InterPro; IPR000242; Tyr_PP.
CC Pfam; PF00017; SH2; 2.
CC Pfam; PF00102; Y_phosphatase; 1.
CC PRINTS; PR00700; PTPHPHASE.
CC PRINTS; PR00401; SH2DOMAIN.
CC ProDom; PD000093; SH2; 2.
CC SMART; SM00194; PTPC; 1.
CC SMART; SM00252; SH2; 2.
CC PROSITE; PS00001; SH2; 2.
CC PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
CC PROSITE; PS00056; TYR_PHOSPHATASE 2; 1.
CC PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
CC KW Hydrolase; SH2 domain; Repeat.
CC FT DOMAIN 6 102 SH2 1.
CC FT DOMAIN 112 215 SH2 2.
CC FT DOMAIN 246 517 PROTEIN-TYROSINE PHOSPHATASE (BY
CC FT ACT_SITE 455 PHOSPHOCYSTEINE INTERMEDIATE (BY
CC FT SIMILARITY).
CC SQ SEQUENCE 613 AA; 69578 MW; 29364B22B8F45C87 CRC64;
Query Match 19.9%; Score 482.5; DB 1; Length 613;
Best Local Similarity 36.9%; Pred. No. 4.5e-26;
Matches 108; Conservative 52; Mismatches 104; Indels 29; Gaps 8;
QY 22 EGAVLG---EFSDIQACSAANKADGVCSTVAGSRPENVRKRYKDVLPDQTVILSL 78
DB 239 EDTAKAGFEWEEFESLQ---KQEAKNLHQRLEGQRPENKSKRYKNILPFOHSVIL--- 291
QY 79 QEEGH-----SDYINGNFIQV-----DGLAVIATQGLPHTLLDFWRLWVEFGVKY 127
DB 292 --QGRDSNIPGSDYINANYRNQLLGPDENSKTVIASQCLDATTVDNFQWAGWENTRVI 349
QY 128 LMACREIENGKRCERYWAQEQPLQGLFCITLKEKWLNEIDIMLRTLVTFQKE--- 184
DB 350 VMTTEVEKGRKCVYPYWPVGTQRYVGLYSVTNCKEHDTAZ-YKLRLTQISPLDNGDLV 408
QY 185 RSVYQLQYMSWPRGVPSSPDHMLAMVEEARLQSGPE--PLCVHCSAGCGRTGVLCV 242
DB 409 REIMHYQLSWPDHSPVPSSLLAFVELVQEVKATQKG--PILVHCSAGVGRITGF 468
QY 243 DVYRQLLLTQMIIPDPSLFDVVLKQKQRAAVQTEQRYFLYHTVAQFCT 295
DB 469 DMLMESVSTKGLDCLDIDIKTIQWRAQSGWQTEAQYKFIYVLAQFIET 521
RESULT 8
PTN6_MOUSE STANDARD; PRT; 595 AA.
ID P29351; Q35128; Q63872; Q63873; Q63874; Q921G3; Q9QVA6; Q9QVA7;
AC Q9QVA8; Q9QVA9;
DT 01-DEC-1992 (Rel. 24, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 6 (EC 3.1.3.48)
DE (Protein-tyrosine phosphatase 1C) (PTP-1C) (Hematopoietic cell
DE protein-tyrosine phosphatase)
DE (Protein-tyrosine phosphatase)
DE PTPN6 OR PTP1C OR HCP OR HCPH.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=DBA/2; PubMed=1732748;
RA MEDLINE=92123209; PubMed=1732748;
RX Yi T., Cleveland J.L., Ihle J.N.;
RA "Protein tyrosine phosphatase containing SH2 domains:
RT characterization, preferential expression in hematopoietic cells, and
RT localization to human chromosome 12p12-p13";
RL Mol. Cell. Biol. 12:836-846(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92236615; PubMed=1373816;
RA Matthews R.J., Bowne D.B., Flores E., Thomas M.L.;
RA "Characterization of hematopoietic intracellular protein tyrosine
RT phosphatases: description of a phosphatase containing an SH2 domain
RT and another enriched in proline-, glutamic acid-, serine-, and
RT threonine-rich sequences";
RL Mol. Cell. Biol. 12:2396-2405(1992).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANTS MOTHEATEN AND VIABLE MOTHEATEN.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RX MEDLINE=93113972; PubMed=8324828;
RA Schultz L.D., Schweitzer P.A., Rajan T.V., Yi T., Ihle J.N.,
RA Matthews R.J., Thomas M.L., Beier D.R.;
RT "Mutations at the murine motheaten locus are within the hematopoietic
RT cell protein-tyrosine phosphatase (Hcph) gene";
RL Cell 73:1445-1454(1993).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 3).
RX MEDLINE=98112780; PubMed=9445485;
RA Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
RA Lu J., Gorrell J.H., Chinnault A.C., Belmont J.W., Miller W.,
RA Gibbs R.A.;
RT "Comparative sequence analysis of a gene-rich cluster at human
RT chromosome 12p13 and its syntenic region in mouse chromosome 6";
RL Genome Res. 8:29-40(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND SUBUNIT.
RC STRAIN=C3H; TISSUE=Adrenal gland;
RX MEDLINE=99348302; PubMed=10419485;
RA Martin A., Teui H.W., Shulman M.J., Iseman D., Tsui F.W.;
RA "Murine SHP-1 splice variants with altered Src homology 2 (SH2)
RT domains. Implications for the SH2-mediated intramolecular regulation
RT of SHP-1";
RL J. Biol. Chem. 274:21725-21734(1999).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE=2389257; PubMed=12477932;
RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bheh N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEvan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [7]
RP SEQUENCE OF 54-68; 128-135; 137-151; 242-252; 278-285; 293-308 AND
RP 373-382, AND PHOSPHORYLATION
RX MEDLINE=93054686; PubMed=1385421;
RA Yeung Y.-G., Berg K.L., Pixley F.J., Angeletti R.H., Stanley E.R.;
RT "Protein tyrosine phosphatase-1C is rapidly phosphorylated in tyrosine
RT in macrophages in response to colony stimulating factor-1";

J. Biol. Chem. 267:23447-23450(1992).
[8]
INTERACTION WITH PTPNS1.
MEDLINE=98380500; PubMed=9712903;
Veillette A., Thibaud E., Latour S.;
"High expression of inhibitory receptor SHPS-1 and its association
with protein tyrosine phosphatase SHP-1 in macrophages";
J. Biol. Chem. 273:22719-22728(1998).
FUNCTION: plays a key role in hematopoiesis. This PTPase activity
may directly link growth factor receptors and other signaling
proteins through protein-tyrosine phosphorylation. The SH2 regions
may interact with other cellular components to modulate its own
phosphatase activity against interacting substrates.
CAVATYRIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
tyrosine + phosphate.
SUBUNIT: Monomer. Binds PTPNS1.
SUBCELLULAR LOCATION: Cytoplasmic.
ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
Name=1;
IsoId=P29351-1; Sequence=Displayed;
Name=2;
IsoId=P29351-2; Sequence=VSP_0051131;
Name=3;
IsoId=P29351-3; Sequence=VSP_005132, VSP_005133;
TISSUE SPECIFICITY: Expressed predominantly in hematopoietic
cells.
PTM: Phosphorylated on tyrosine residues.
SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
Non-receptor class subfamily.
SIMILARITY: Contains 2 SH2 domains.
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EMBL; M68902; AAA37796.1; -;
EMBL; M90389; AAA40007.1; -;
EMBL; S63763; -; NOT_ANNOTATED_CDS.
EMBL; S63764; -; NOT_ANNOTATED_CDS.
EMBL; S63803; -; NOT_ANNOTATED_CDS.
EMBL; AC002397; AAC36009.1; -;
EMBL; AC002397; AAC36008.1; -;
EMBL; U65955; AAD00152.1; -;
EMBL; U65952; AAD00152.1; JOINED.
EMBL; U65953; AAD00152.1; JOINED.
EMBL; U65954; AAD00152.1; JOINED.
EMBL; U65955; AAD00152.1; -;
EMBL; U65951; AAD00151.1; -;
EMBL; U65952; AAD00151.1; JOINED.
EMBL; U65953; AAD00151.1; JOINED.
EMBL; U65954; AAD00151.1; JOINED.
EMBL; BC012660; AAH12660.1; -;
HSP; P29350; IGWZ.
MGD; MGI:96055; Hcph.
InterPro; IPR000980; SH2.
InterPro; IPR000387; TYR_phosphatase.
InterPro; IPR000242; Tyr_PP.
Pfam; PF00017; SH2; 2.
Pfam; PF00102; Y_phosphatase; 1.
PRINTS; PR00700; PRTYPHEPTASE.
PRINTS; PR00401; SH2DOMAIN.
ProDom; PD000093; SH2; 2.
SMART; SM00194; PTPC; 1.
SMART; SM00252; SH2; 2.
PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
PROSITE; PS00566; TYR_PHOSPHATASE_2; 1.
PROSITE; PS00055; TYR_PHOSPHATASE_FTP; 1.
PROSITE; PS00001; SH2; 2.

KW Hydrolase; SH2 domain; Repeat; Phosphorylation; Alternative splicing.
 FT DOMAIN 4 100 SH2 1.
 FT DOMAIN 110 213 SH2 2.
 FT DOMAIN 269 514 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 453 PHOSPHOCYSTEINE INTERMEDIATE (BY
 SIMILARITY).
 FT VARSPLIC 1 3 MVR -> MLESG (in isoform 2).
 FT VARSPLIC 1 39 /FTid=VSP_005131.
 FT VARSPLIC 40 44 Missing (in isoform 3).
 FT VARSPLIC 40 44 /FTid=VSP_005132.
 FT VARSPLIC 40 44 SLSVR -> MLESG (in isoform 3).
 FT VARSPLIC 40 44 /FTid=VSP_005133.
 FT VARSPLIC 40 44 EYVTOGQILQDRGTIIHLKYP -> VPRPHIWRAGGVTA
 FT VARSPLIC 40 44 AGQGRALD (IN MOTHEATEN (ME)).
 FT VARSPLIC 40 44 MISSING (IN MOTHEATEN (ME)).
 FT VARSPLIC 40 44 A -> R (IN REF. 1 AND 3).
 FT VARSPLIC 40 44 K -> Q (IN REF. 1 AND 3).
 FT VARSPLIC 40 44 E -> D (IN REF. 6).
 SQ SEQUENCE 595 AA; 67559 MW; CFI7300D032638D2 CRC64;

Query Match
 Best Local Similarity 19.6%; Score 475.5; DB 1; Length 595;
 Matches 106; Conservative 53; Mismatches 105; Indels 29; Gaps 8;

QY 22 EGAVLAG---EFSDIQACSAWKGADGVCSTVAGSRPENVRKNRYKDVLPDQTRVLSLL 78
 DB 237 EDTAKAGWEEFESLQ---KQEVKNLHORLEGORPENKSKNRYKNILPFDHGRVIL--- 289
 QY 79 QEEGH-----SDYINGNFRGV-----DGLAYIAHQPLPHTLDFWELWEPGVKVI 127
 DB 290 --QQRSDNIPGSDYINANYKNQLLGPDENSKTYIASQGCLDATVDFWQAWQENRVI 347
 QY 128 LMACREIENGKRCERYMAQOEPLQGLFCITILKEKWLNEIMRLTKLVTPKES--- 184
 DB 348 VMTREVEKGNKCVYWPVGTVGVVGLSVNREHDTAE-YKLTQLQISPLDNGDLV 406
 QY 185 RSVTQLOQWPDGRVSSPDHMLAMVEARRLQSGPE--PLCVHCSAGCGRTGVLCV 242
 DB 407 REIWHYQYLSWPDHGVSEPGVLSFLQINQORQESLPHAGPIVHCSAGIGRTGIIVI 466
 QY 243 DYVQQLLLTOMIPDFSLFDVLKWRQRPAAVQTEQYRFLVHTVAQMFCT 295
 DB 467 DLMESISTKGLDCDDIDIKTIQVWRAQRSGMVQTEAQYKFIYVAIAQFIET 519

RESULT 9
 PTPV RAT
 ID -PTPV RAT
 AC Q64612; STANDARD; PRT; 1711 AA.
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Receptor-type protein-tyrosine phosphatase V precursor (EC 3.1.3.48)
 DE (Embryonic stem cell protein-tyrosine phosphatase) (ES cell
 phosphatase) (Osteotesticular protein-tyrosine phosphatase) (OST-PTP).
 DE PTPRV OR ESP.
 GN Rattus norvegicus (Rat).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Osteosarcoma;
 RA MEDLINE=95074080; PubMed=7527035;
 RA Mauro L.J., Olmsted E.A., Skrobacz B.M., Mourey R.J., Davis A.R.,
 RA Dixon J.E.;
 RA "Identification of a hormonally regulated protein tyrosine
 RT phosphatase associated with bone and testicular differentiation."
 RL J. Biol. Chem. 269:30659-30667(1994).
 CC -/- FUNCTION: May function in signaling pathways during bone
 CC remodeling, as well as serve a broader role in cell interactions
 CC associated with differentiation in bone and testis. Optimal pH for
 CC phosphatase activity is 5.6. Associated with differentiation in

bone and testis.
 CC -/- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
 CC tyrosine + phosphate.
 CC -/- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -/- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=A presumed alternate transcript of 4.8-5.0 kilobases,
 CC which may lack PTP domains, is present in proliferating
 CC osteoblasts, but not detectable at other stages;
 CC Name=1;
 CC IsoId=Q64612-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q64612-2; Sequence=Not described;
 CC Note=No experimental confirmation available;
 CC -/- TISSUE SPECIFICITY: Bone and testis. In the latter, restricted to
 CC the basal portion of the seminiferous tubule.
 CC -/- DEVELOPMENTAL STAGE: Up-regulated in differentiating cultures of
 CC primary osteoblasts and down-regulated in late stage mineralizing
 CC cultures. In testis, expression is highest between stages I and
 CC VII when maturing spermatids remain buried within the sertoli
 CC epithelium.
 CC -/- INDUCTION: By parathyroid hormone and cAMP analogs.
 CC -/- PTM: The cytoplasmic domain contains potential phosphorylation
 CC sites.
 CC -/- SIMILARITY: Contains 2 protein-tyrosine phosphatase domains.
 CC -/- SIMILARITY: Contains 10 fibronectin type III domains.
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 CC -----
 CC EMBL; L36884; AAA63911.1; -;
 CC HSP; F18052; LYFO.
 CC InterPro; IPR008957; FN III-like.
 CC InterPro; IPR003961; FN III.
 CC InterPro; IPR00387; TVR phosphatase.
 CC InterPro; IPR000242; Tyr_PP.
 CC Pfam; PF00041; fn3; 7
 CC Pfam; PF0102; Y_phosphatase; 1.
 CC PRINTS; PR00700; PTPPHPTASE.
 CC SMART; SM00060; FN3; 8.
 CC SMART; SM00194; PTPC; 1.
 CC PROSITE; PS00383; TVR_PHOSPHATASE_1; 1.
 CC PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
 CC PROSITE; PS00055; TYR_PHOSPHATASE_Ptp; 2.
 CC Hydrolase; Transmembrane; Repeat; Signal; Glycoprotein;
 KW Alternative splicing.
 FT SIGNAL 1 17
 FT CHAIN 18 1711
 FT POTENTIAL.
 FT RECEPTOR-TYPE PROTEIN-TYROSINE
 FT PHOSPHATASE V.
 FT EXTRACELLULAR (POTENTIAL).
 FT POTENTIAL.
 FT CYTOPLASMIC (POTENTIAL).
 FT FIBONECTIN TYPE-III 1.
 FT FIBONECTIN TYPE-III 2.
 FT FIBONECTIN TYPE-III 3.
 FT FIBONECTIN TYPE-III 4.
 FT FIBONECTIN TYPE-III 5.
 FT FIBONECTIN TYPE-III 6.
 FT FIBONECTIN TYPE-III 7.
 FT FIBONECTIN TYPE-III 8.
 FT FIBONECTIN TYPE-III 9.
 FT FIBONECTIN TYPE-III 10.
 FT PROTEIN-TYROSINE PHOSPHATASE 1.
 FT PROTEIN-TYROSINE PHOSPHATASE 2.
 FT PHOSPHOCYSTEINE INTERMEDIATE (BY
 FT SIMILARITY).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 42 42
 FT CARBOHYD 74 74

receptor-mediated signaling in monocytes.";
 Eur. J. Immunol. 28:3423-3434(1998).
 [11]
 RN INTERACTION WITH PTPNS1.
 RA MEDLINE=98380500; PubMed=9712903;
 RA Veillette A., Thibaut E., Latour S.;
 RT "High expression of inhibitory receptor SHPS-1 and its association
 RT with protein tyrosine phosphatase SHP-1 in macrophages.";
 RL J. Biol. Chem. 273:22719-22728(1998).
 [12]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 248-399.
 RX MEDLINE=9847672; PubMed=9774441;
 RA Yang J., Liang X., Niu T., Meng W., Zhao Z., Zhou G.W.;
 RT "Crystal structure of the catalytic domain of protein-tyrosine
 RT phosphatase SHP-1.";
 RL J. Biol. Chem. 273:28199-28207(1998).
 CC -!- FUNCTION: Plays a key role in hematopoiesis. This PTPase activity
 CC may directly link growth factor receptors and other signaling
 CC proteins through protein-tyrosine phosphorylation. The SH2 regions
 CC may interact with other cellular components to modulate its own
 CC phosphatase activity against interacting substrates.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphatase + H(2)O = protein
 CC tyrosine + phosphate.
 CC -!- SUBUNIT: Monomer (By similarity). Binds PTPNS1, LILRB1 and LILRB2.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=Long;
 CC IsoId=P29350-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=P29350-3; Sequence=VSP_007775;
 CC Name=3; Synonyms=Short;
 CC IsoId=P29350-2; Sequence=VSP_005129; VSP_005130;
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in hematopoietic
 CC cells.
 CC -!- PM: Phosphorylated on serine and tyrosine residues.
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
 CC Non-receptor class subfamily.
 CC -!- SIMILARITY: Contains 2 SH2 domains.
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 CC -----
 DR EMBL; M74903; AAA35963.1; -;
 DR EMBL; X62055; CAA43982.1; -;
 DR EMBL; M7273; AAA36610.1; -;
 DR EMBL; U15528; AAA82880.1; -;
 DR EMBL; U15536; AAA82880.1; JOINED.
 DR EMBL; U15535; AAA82880.1; JOINED.
 DR EMBL; U15534; AAA82880.1; JOINED.
 DR EMBL; U15533; AAA82880.1; JOINED.
 DR EMBL; U15532; AAA82880.1; JOINED.
 DR EMBL; U15531; AAA82880.1; JOINED.
 DR EMBL; U15530; AAA82880.1; JOINED.
 DR EMBL; U15529; AAA82880.1; JOINED.
 DR EMBL; U15528; AAA82880.1; JOINED.
 DR EMBL; U15537; AAA82879.1; JOINED.
 DR EMBL; U15535; AAA82879.1; JOINED.
 DR EMBL; U15534; AAA82879.1; JOINED.
 DR EMBL; U15533; AAA82879.1; JOINED.
 DR EMBL; U15532; AAA82879.1; JOINED.
 DR EMBL; U15531; AAA82879.1; JOINED.
 DR EMBL; U15530; AAA82879.1; JOINED.
 DR EMBL; U15529; AAA82879.1; JOINED.
 DR EMBL; U47924; AAB51323.1; -;
 DR EMBL; U47924; AAB51322.1; -;
 DR EMBL; BC002523; AAB02523.1; -;
 DR EMBL; BC007667; AAB07667.1; -;

DR PIR; B42031; S20825.
 DR PDB; 1GWZ; 22-AUG-99.
 DR PDB; 1FPR; 07-MAR-01.
 DR Genew; HGNC:9658; PTPN6.
 DR MIM; 176883; -;
 DR GO; GO:0016020; C:membrane; TAS.
 DR GO; GO:0004725; P:protein tyrosine phosphatase activity; TAS.
 DR GO; GO:0006913; P:apoptosis; TAS.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR003595; PTPc_motif.
 DR InterPro; IPR000980; SH2_motif.
 DR InterPro; IPR00387; TYR_phosphatase.
 DR InterPro; IPR00242; TYR_PP.
 DR Pfam; PF00017; SH2; 2.
 DR PRINTS; PR00102; Y_phosphatase; 1.
 DR PRINTS; PR00700; PRTYPHPTASE.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR ProDom; PD000093; SH2; 2.
 DR SMART; SM00194; PTPC; 1.
 DR SMART; SM00404; PTPC_motif; 1.
 DR SMART; SM00252; SH2; 2.
 DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
 DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
 Query Match 19.1%; Score 463; DB 1; Length 595;
 Best Local Similarity 32.9%; Pred. No. 9.6e-25;
 Matches 112; Conservative 56; Mismatches 110; Indels 62; Gaps 10;
 QY 22 EGAVLAG---EFSDIQACSAAWKAGVCGSTVAGSRPENVRKRYKDLVPYDQTRVLSLL 78
 DB 237 EDTAKAGWEEFESLQ-----KQEVKNLQRLQEGQRPENKGRYKNILPFDHSVIL--- 289
 QY 79 QEEGH-----SDYINGNFIRGV-----DGLAYIATQGLPHLLDFWRLVWFGVKVI 127
 DB 290 --QGRSDSNIPGSDYINANYIKNQLLGPDENAKTVIASQGLEATVDFWQMAWQENSRVI 347
 QY 128 LMACREIENGRKRCERYWAQEPQLQGLFCITLIKELWLNEDIMLRITLVTFOKES--- 184
 DB 348 VMTTEVEKGRKVCVPYFVGMQRAYGYSVTNCGEHDITE-YKLRLQVSLDNGDLI 406
 QY 185 RSVQLQVMSWPDGVPSSPDHMLAMVEEARLQSGSPE--PLCVHCSAGCGRTGVLCTV 242
 DB 407 REIHWYQLSWPDGVPSEPGVLSFLDQINQROESLPHAGPIIVHCSAGIGRTGTIIV 466
 QY 243 DYVRGLLTOMIPDFSLFDVVLKVRKORPAAVQTEEQYRFLYHTVAQMFCT----- 295
 DB 467 DMLMENISTKGLDCDDIDIOKTIQWRAQRSGMVQTEAQYKFIYVAIAQFIETTKKLEVL 526
 QY 296 -----LQNA-----SPHYQNIKEN 309
 DB 527 OSQKQSEYSEGNITPPAMKVAAKAGRTSSKHEDVYEN 566
 RESULT 11
 PTPN4 HUMAN
 ID PTPN4 HUMAN STANDARD; PRT; 926 AA.
 AC P29074;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein tyrosine phosphatase, non-receptor type 4 (EC 3.1.3.48)
 DE (Protein-tyrosine phosphatase MEG1) (PTPase-MEG1) (MEG).
 GN PTPN4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91288564; PubMed=1648233;
 RA Gu M., York J.D., Warshawsky I., Majerus P.W.;

RT RT protein-tyrosine-phosphatase with sequence homology to cytoskeletal protein 4.1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 88:5867-5871(1991).
 RN [2]
 RC SEQUENCE FROM N.A.
 RP TISSUE=Colon;
 RX MEDLINE=22389257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Srapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: May act at junctions between the membrane and the cytoskeleton.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
 CC -!- SIMILARITY: Contains 1 FERM domain.
 CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Non-receptor class subfamily.
 CC -----
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 CC -----
 DR EMBL; M68941; AAA36530.1; -;
 DR EMBL; BC010674; AAA10674.1; -;
 DR PIR; A41105; A41105.
 DR HSP; P29350; 1GWZ.
 DR Genew; HGNC:9656; PTPN4.
 DR MIM; 176878; -;
 DR GO; GO:0005737; Cytoplasm; TAS.
 DR GO; GO:0004726; F:non-membrane spanning protein tyrosine phosphatase.
 DR GO; GO:0006470; P:protein amino acid dephosphorylation; TAS.
 DR InterPro; IPR000299; Band_4.1.
 DR InterPro; IPR01478; PDZ.
 DR InterPro; IPR00387; TYR phosphatase.
 DR Pfam; PF00373; Band_41; 1.
 DR Pfam; PF00595; PDZ; 1.
 DR Pfam; PF00102; Y_phosphatase; 1.
 DR PRINTS; PR00935; BAND41.
 DR PRINTS; PR00700; PRTYRPHATASE.
 DR SMART; SM00295; B41; 1.
 DR SMART; SM00228; PDZ; 1.
 DR SMART; SM00194; PTPC; 1.
 DR PROSITE; PS00660; FERM_1; 1.
 DR PROSITE; PS00661; FERM_2; 1.
 DR PROSITE; PS00057; FERM_3; 1.
 DR PROSITE; PS01066; PDZ; 1.
 DR PROSITE; PS00383; TYR PHOSPHATASE 1; 1.
 DR PROSITE; PS00056; TYR PHOSPHATASE 2; 1.
 DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.

KW Structural protein; Cytoskeleton; Hydrolase.
 FT DOMAIN 29 312 FERM.
 FT DOMAIN 517 589 PDZ.
 FT DOMAIN 677 926 PROTEIN-TYROSINE PHOSPHATASE.
 FT ACT_SITE 852 852 PHOSPHOCYSTEINE INTERMEDIATE (BY SIMILARITY).
 SQ SEQUENCE 926 AA; 105911 MW; 4DAC6A87A675CPB0 CRC64;
 Query Match 19.1%; Score 462; DB 1; Length 926;
 Best Local Similarity 37.6%; Pred. NO. 1.9e-24;
 Matches 106; Conservative 47; Mismatches 107; Indels 22; Gaps 9;
 QY 17 ARGREGAVLAGEPSDIOACSAAKADGVCSTVAGSRPENVRKRYKDVLPYDQTRVILS 76
 DB 647 AEGLITGVLT-QFDLYR-----KKPGWTWSA-KLQNKISKNRYRDISPYDAFRVIL- 698
 QY 77 LLOEGHSDYINGNPIRGVDSGLA-----YIATQGLPHTLLDFWELVWFGVKVLMACR 132
 DB 699 -----KGNEDYINANYINMEIPSSIIQYIAQCGLPHTCTDFWQMTWEGSSVMVLT 754
 QY 133 ELENKRCERYWAOEPLQGLFCITLKEKLNEDIMLRLTKLVTPQK--ESRSVYQL 190
 DB 755 QVERGRVKCHQWPEPTGSSSGYQVTCHEEG-NTAYIFKMTLFNQKNESEPLTQI 813
 QY 191 QYMSWPFDRGVSSPDHMLAMVBEARRLQSGPEPLCVHCSAGCGRTGLVCTVDVYRQLLL 250
 DB 814 QYIAPDHGVDDSSDFLDFVCHVRNKRAGKEPVPVHCSAGIGRTGLVITME--TAMCL 871
 QY 251 TQMIPTDFSLFDVVLKMRKORPAAVQTEOYRFLVHTVAQMF 292
 DB 872 IECNQPVPL-DIVRTMRDQRAMMIQTQSYRFXVCEAILKVY 912
 RESULT 12
 PTNB-CHICK STANDARD; PRT; 593 AA.
 AC Q90687;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Protein-tyrosine phosphatase, non-receptor type 11 (EC 3.1.3.48) (CSH-FP2).
 DE PTPN11 OR SH-PTP2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Erythroblast;
 RX MEDLINE=97080506; PubMed=8921851;
 RA Park C.Y., LaMontagne K.R., Tonks N.K., Hayman M.J.;
 RT "Cloning and expression of the chicken protein tyrosine phosphatase SH-PTP2";
 RL Gene 177:93-97(1996).
 CC -!- FUNCTION: This PTPase activity may directly link growth factor receptors and other signaling proteins through protein-tyrosine phosphorylation. The SH2 regions may interact with other cellular components to modulate its own phosphatase activity against interacting substrates (By similarity). May play a positive role during the stages of erythroid cell proliferation.
 CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein tyrosine + phosphate.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in embryonic fibroblast, hematopoietic, erythroid, myeloid and lymphoid cells.
 CC -!- PTM: Phosphorylated by tyrosine-protein kinases (By similarity).
 CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family. Non-receptor class subfamily.
 CC -!- SIMILARITY: Contains 2 SH2 domains.
 CC -----
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RP ERATUM.
RA Tartaglia M., Mehler E.L., Goldberg R., Zampino G., Brunner H.G.,
RA Krenner H., van der Burgt I., Crosby A.H., Ion A., Jeffery S.,
RA Kalidas K., Patton M.A., Kucherlapati R.S., Gelb B.D.;
RL Nat. Genet. 29:491-491(2001).
RN [11]
RP ERATUM.
RA Tartaglia M., Mehler E.L., Goldberg R., Zampino G., Brunner H.G.,
RA Krenner H., van der Burgt I., Crosby A.H., Ion A., Jeffery S.,
RA Kalidas K., Patton M.A., Kucherlapati R.S., Gelb B.D.;
RL Nat. Genet. 30:123-123(2001).
RN [12]
RP VARIANTS NS ALA-42; ALA-60; ASN-61; GLY-72; ASP-62; CYS-63; GLY-72;
RP ILE-73; ASP-76; ARG-79; ALA-106; ASP-139; CYS-279; VAL-282; LEU-285;
RP SER-285; ASP-308; SER-308; VAL-309; LYS-501 AND VAL-504, AND VARIANT
RP NOONAN-LIKE SYNDROME SER-308.
RX MEDLINE=21987645; PubMed=11992261;
RA Tartaglia M., Kalidas K., Shaw A., Song X., Musat D.R.,
RA van der Burgt I., Brunner H.G., Bertola D.R., Crosby A.H., Ion A.,
RA Kucherlapati R.S., Jeffery S., Patton M.A., Gelb B.D.;
RT "PTPN11 mutations in Noonan syndrome: molecular spectrum, genotype-
RT phenotype correlation, and phenotypic heterogeneity";
RL Am. J. Hum. Genet. 70:1555-1563(2002).
RN [13]
RP VARIANTS LEOPARD SYNDROME CYS-279 AND MET-468.
RX MEDLINE=22104852; PubMed=12058348;
RA Digilio M.C., Conti E., Sarkozy A., Mingarelli R., Dotterini T.,
RA Marino B., Pizzuti A., Dallapiccola B.;
RT "Grouping of multiple-lentiginos/LEOPARD and Noonan syndromes on the
RT PTPN11 gene";
RL Am. J. Hum. Genet. 71:389-394(2002).
RN [14]
RP VARIANTS NS ASP-62; CYS-63 AND THR-502.
RX MEDLINE=22236043; PubMed=12325025;
RA Maheshwari M., Belmont J., Fernbach S., Ho T., Molinari L., Yakub I.,
RA Yu F., Combes A., Towbin J., Craig W.J., Gibbs R.;
RT "PTPN11 mutations in Noonan syndrome type I: detection of recurrent
RT mutations in exons 3 and 13";
RL Hum. Mutat. 20:298-304(2002).
RN [15]
RP VARIANTS NS GLY-61; CYS-63; SER-72; ILE-73; SER-285 AND ASP-308.
RX MEDLINE=22151235; PubMed=12161469;
RA Kosaki K., Suzuki T., Muroya K., Hasegawa T., Sato S., Matsuo N.,
RA Kosaki R., Nagai T., Muroya K., Hasegawa Y., Ogata T.;
RT "PTPN11 (protein-tyrosine phosphatase, nonreceptor-type 11) mutations
RT in seven Japanese patients with Noonan syndrome";
RL J. Clin. Endocrinol. Metab. 87:3529-3533(2002).
RN [16]
RP VARIANTS JMML TYR-61; VAL-61; LYS-69; THR-72; VAL-72; ALA-76; GLY-76;
RP LYS-76; VAL-76; ALA-503 AND ARG-503, VARIANTS MYELODYSPLASTIC SYNDROME
RP VAL-60; VAL-61; LYS-69; LEU-71 AND ALA-76, VARIANTS NS ASP-62 AND
RP ILE-73, AND VARIANT ACUTE MYELOID LEUKEMIA LYS-71.
RX MEDLINE=22660528; PubMed=12717436;
RA Tartaglia M., Niemeyer C.M., Fragale A., Song X., Buechner J.,
RA Jung A., Haehlen K., Hasle H., Licht J.D., Gelb B.D.;
RT "Somatic mutations in PTPN11 in juvenile myelomonocytic leukemia,
RT myelodysplastic syndromes and acute myeloid leukemia";
RL Nat. Genet. 34:148-150(2003).
CC -!- FUNCTION: This PTPase activity may directly link growth factor
CC receptors and other signaling proteins through protein-tyrosine
CC phosphorylation. The SH2 regions may interact with other cellular
CC components to modulate its own phosphatase activity against
CC interacting substrates.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBUNIT: Binds PTPNS1.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: Widely expressed, particularly abundant in
CC heart, brain, and skeletal muscle.
CC -!- PTM: Phosphorylation of tyrosine residues at the C-terminus by
CC platelet-derived growth factor creates a binding site for the SH2
CC domain of GRB2.
CC -!- DISEASE: Defects in PTPN11 are the cause of LEOPARD syndrome

[MIM:151100], an autosomal dominant disorder allelic with Noonan
syndrome. The acronym LEOPARD stands for lentiginos,
electrocardiographic conduction abnormalities, ocular
hypertelorism, pulmonic stenosis, abnormalities of genitalia,
retardation of growth, and deafness.
-!- DISEASE: Defects in PTPN11 are a cause of Noonan syndrome (NS)
[MIM:163950]; also designated Noonan syndrome 1 (NS1). NS is an
autosomal dominant disorder characterized by dysmorphic facial
features, short stature, hypertelorism, cardiac anomalies,
deafness, motor delay, and a bleeding diathesis. It is a
genetically heterogeneous and relatively common syndrome, with an
estimated incidence of 1 in 1000-2500 live births. Mutations in
PTPN11 account for more than 50% of the cases. Rarely, NS is
associated with juvenile myelomonocytic leukemia (JMML).
-!- DISEASE: Defects in PTPN11 are a cause of Noonan-like syndrome
[MIM:163955]; also known as Noonan-like/multiple giant cell lesion
syndrome. It is an autosomal dominant disorder characterized by
Noonan features associates with giant cell lesions of bone and
soft tissue.
-!- DISEASE: Defects in PTPN11 are a cause of juvenile myelomonocytic
leukemia (JMML) [MIM:607785], a pediatric myelodysplastic syndrome
that constitutes approximately 30% of childhood cases of
myelodysplastic syndrome (MDS) and 2% of leukemia.
-!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC -!- SIMILARITY: Contains 2 SH2 domains.
CC -----
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CC or send an email to license@isb-sib.ch.
CC -----
CC ENBL; L08807; ; NOT ANNOTATED_CDS.
DR ENBL; X70766; CAA50045.1; -
DR ENBL; D13540; BAA02740.2; -
DR ENBL; L07527; AAA17022.1; -
DR ENBL; L03535; AAA36611.1; -
DR PIR; JN0805; JN0805.
DR PDB; 2SH2; 16-FEB-99.
DR Genew; HGNC:9644; PTPN11.
DR MIM; 176876; -
Query Match 18.7%; Score 453; DB 1; Length 593;
Best Local Similarity 33.8%; Pred. No. 4.7e-24;
Matches 119; Conservative 53; Mismatches 126; Indels 54; Gaps 12;
Qy 1 MRSLSASFLERLEARGREGAVLA-----GEPSDI--QACSAANKADGVCS 47
Db 212 LKQPLNTTRINAABIESR-VRELSKLAETTDVKQGFMEFETLQOQCECKLLY-----S 264
Qy 48 TVAGSRPNVKNRYKDVLPYDQTRVILSLQEGH-----SDYINGNFI-----RG 94
Db 265 RKEGQEQENKNRYKNILPFDHTRVL-----HDGDPNPEVSDYINANIIMPEFTKCNN 320
Qy 95 VDGLSAYIATQGPLHTLLDFWRLVWFGVKVILMACREIENGRKCRERYAQOEPLQT 154
Db 321 SPKPKSVIATQGLQNTVDFWVFNQENSRVIVMTTKEVERGSKCKVKYVDEVALKEY 380
Qy 155 GLFCITLIEKWLNEDIMLRLTKVTFQKE---SRSVYQLQVMSWPDGRGVSPSPDHMLAVY 211
Db 381 GVMNRVNVKES-AAHDYTLRELKLSKVGQGNTERVTWQYHFTWPDHGVSPDPGGVLDPL 439
Qy 212 EEARRLQGS--GFPEPLCVHCSAGCGRTGLVCTDVYVYRQLLLTQMTPPPDFSLFDVVLKMRK 269
Db 440 EEVHHQESIMDAGPVVHCSAGIGRTGTFIVILIDILIREKGVDCDIDVPTKIOMVRS 499
Qy 270 QRPAAVTQTEQVRFYHTYAQMFCSTLQ-----NASHYQNIKENCA 311
Db 500 QRSQMVTQAVRFYIMAV-QHYIETLQRRIEEOKSKKKGHEYNINIKYSLA 550

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RESULT 14
PTNB MOUSE
ID PTNB MOUSE STANDARD; PRT; 585 AA.
AC P35235;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, last sequence update)
DT 10-OCT-2003 (Rel. 42, last annotation update)
DE Protein-tyrosine phosphatase, non-receptor type 11 (BC 3.1.3.48)
DE (Protein-tyrosine phosphatase SYP).
GN PTPN11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN [2]
RN [3]
SEQUENCE FROM N.A.
RP MEDLINE=93206094; PubMed=8096088;
RA Feng G.-S., Hui C.-C., Pawson T.;
RT "SH2-containing phosphotyrosine phosphatase as a target of protein-
RL tyrosine kinases.";
RL Science 259:1607-1611(1993).
RN [2]
RN [3]
PTPNS1 BINDING.
RP MEDLINE=97215901; PubMed=9062191;
RA Kharitonov A., Chen Z., Sures I., Wang H., Schilling J.,
RA Ullrich A.;
RT "A family of proteins that inhibit signalling through tyrosine kinase
RL receptors.";
RL Nature 386:181-186(1997).
RN [3]
X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS) OF 4-103.
RP MEDLINE=94363243; PubMed=7521735;
RA Lee C.-H., Kominos D., Jacques S., Margolis B., Schlessinger J.,
RA Shoelson S.E., Kuriyan J.;
RT "Crystal structures of peptide complexes of the amino-terminal SH2
RL domain of the SYP tyrosine phosphatase.";
RL Structure 2:423-438(1994).
CC -!- FUNCTION: This PTPase activity may directly link growth factor
CC receptors and other signaling proteins through protein-tyrosine
CC phosphorylation. The SH2 regions may interact with other cellular
CC components to modulate its own phosphatase activity against
CC interacting substrates.
CC -!- CATALYTIC ACTIVITY: Protein tyrosine phosphate + H(2)O = protein
CC tyrosine + phosphate.
CC -!- SUBUNIT: Binds PTPNS1.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- PTM: Phosphorylated by tyrosine-protein kinases.
CC -!- SIMILARITY: Belongs to the protein-tyrosine phosphatase family.
CC Non-receptor class subfamily.
CC -!- SIMILARITY: Contains 2 SH2 domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L08663; -; NOT_ANNOTATED_CDS.
CC PIR: A46209; A46209.
CC PDB: 1A1A; 31-AUG-94.
CC PDB: 1A1B; 31-AUG-94.
CC PDB: 1A1C; 31-AUG-94.
CC PDB: 1A1D; 31-AUG-94.
CC MGI: 95511; Ptpn11.
CC GO: 0005515; P:protein binding; IPI.
CC GO: 0007409; P:axogenesis; IMP.
CC GO: 0004801; P:NGF receptor signaling pathway; IMP.
CC InterPro: IPR000980; SH2.
CC InterPro: IPR000387; Tyr_PP.
CC InterPro: IPR00242; Tyr_PP.

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DR Pfam; PF00017; SH2; 2.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PRO0700; PRTYPHPTASE.
DR PRINTS; PRO0401; SH2DOMAIN.
DR ProDom; PD000093; SH2; 2.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00252; SH2; 2.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
DR PROSITE; PS00001; SH2; 2.
KW Hydrolase; SH2 domain; Repeat; Phosphorylation; 3D-structure.
FT DOMAIN 6 102
FT SH2 1.
FT DOMAIN 112 216
FT SH2 2.
FT DOMAIN 216 521
FT PROTEIN-TYROSINE PHOSPHATASE.
FT ACT_SITE 463 463
FT PHOSPHOCYSTEINE INTERMEDIATE (BY
FT SIMILARITY).
FT TURN 5 6
FT STRAND 7 7
FT HELIX 13 22
FT TURN 23 23
FT TURN 26 27
FT STRAND 28 33
FT TURN 38 39
FT TURN 41 47
FT TURN 48 49
FT STRAND 50 55
FT STRAND 57 58
FT STRAND 63 64
FT STRAND 71 71
FT HELIX 74 83
FT TURN 85 86
FT STRAND 89 90
FT TURN 91 92
FT STRAND 95 95
FT STRAND 100 101
FT STRAND 100 101
SQ SEQUENCE 585 AA; 66816 MW; 6CE554F929B8F72A CRC64;
Query Match 18.6%; Score 451; DB 1; Length 585;
Best Local Similarity 31.0%; Pred. No. 6.4e-24;
Matches 128; Conservative 59; Mismatches 142; Indels 84; Gaps 15;
QY 1 MRSLSARSFLERLEARGREGAVLA-----GFSDI--QACSAAWKADGVCS 47
DB 212 LKQPLNTRINAATESR-VRELSKLAETTDKVKQGFWEFEFLQOQCKLLY-----S 264
QY 48 TVAGSRPENVRNRYKDVLPYDQTRVLSLQEEGH-----SDVINGNFI-----RG 94
DB 265 RREGQREQNKRNRYKNILPFDHTEVVL---HDGDPNEPVSIDYINANIIMPEFETKCN 320
QY 95 VDGLSAYATQSGPLPHTLLDFWLVWVEFGVKVILMACREIENGKRCRYWAQOEPLQT 154
DB 321 SKPKKSYATQGLQNTQNTDFWVFNQNSRVVMTTKEVERGSKCVKYPDEYALKEY 380
QY 155 GFICITLKEKWLNEIDMLRTLVKTFOKES-----RSVYQLOVMSWPDGVPSSPDHM 207
DB 381 GVMRVNKNES-AAHYTLRELKUSKQALQGNTERVTWQYHFTWPDHGVSDPGGV 439
QY 208 LAMVEARRLQGS--GPEFLCVHCSAGCGRTGLVTDVYVRQLLLTQMIPDFSLFDVVL 265
DB 440 LDFLEEVHKKQSSIVDAGFVVVHCSAGIGRTGTFIVIDILIDIREKGVDCDIDVPKTIQ 499
QY 266 KVRKORPAVQTEEQRYLYHTVAGMFCSTLQ-----NASPHYQNIKENCAPLYD 315
DB 500 MYRSQSGMVQTEAQRYFIYMAV-QHYLETQRIEIEEQKSKRGHEHTNIR-----YS 552
QY 316 DALFLRTFQALLAIIPRPPGGVLRSGISVSPGSHAMADTYAEFEKRGAPAGAGS 368
DB 553 GELGYTEIRV-----GCFGHSVSP--MDEVGGWVEGLGT 585
RESULT 15
PTNB_RAT

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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:38:19 ; Search time 43 Seconds
(without alignments)
3360.636 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 2424

Sequence: 1 MSRLDSARSFLERLEARGG.....NLIRGPKGPRDPAEWTRV 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_25.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1791.5	73.9	453	11 Q61152	Q61152 mus musculus
2	1782.5	73.5	453	11 Q922E3	Q922E3 mus musculus
3	1775.5	73.2	351	4 Q72637	Q72637 homo sapien
4	1775.5	73.2	372	4 Q8TA96	Q8TA96 homo sapien
5	1754.5	72.4	453	11 P70602	P70602 rattus norv
6	749.5	30.9	802	11 Q7TMP9	Q7TMP9 mus musculus
7	726.5	30.0	799	4 Q9P0J2	Q9P0J2 homo sapien
8	709	29.2	872	4 Q86XU4	Q86XU4 homo sapien
9	706	29.1	775	11 Q80UM4	Q80UM4 mus musculus
10	705.5	29.1	382	11 Q63745	Q63745 rattus norv
11	510.5	21.1	438	11 Q64642	Q64642 rattus norv
12	503.5	20.8	592	13 Q7SV37	Q7SV37 brachydanio
13	498.5	20.6	598	11 Q8BIW7	Q8BIW7 mus musculus
14	491.5	20.3	1118	4 Q15426	Q15426 homo sapien
15	489.5	20.2	1115	4 Q9HD43	Q9HD43 homo sapien
16	485	20.0	1705	11 Q9ERK5	Q9ERK5 mus musculus

17	474.5	19.6	624	4 Q9UK67	Q9UK67 homo sapien
18	471.5	19.5	336	13 Q9IB94	Q9IB94 potamotrygo
19	470	19.4	594	13 Q7ZW17	Q7ZW17 brachydanio
20	469	19.3	926	11 Q9WU22	Q9WU22 mus musculus
21	462	19.1	342	13 Q9IB95	Q9IB95 potamotrygo
22	452	18.6	597	11 Q64509	Q64509 mus musculus
23	449	18.5	292	4 Q8N4S3	Q8N4S3 homo sapien
24	447	18.4	694	13 Q7ZYN2	Q7ZYN2 xenopus lae
25	446.5	18.4	522	5 Q86AJ9	Q86AJ9 dictyosteli
26	445.5	18.4	589	13 Q803M6	Q803M6 brachydanio
27	444	18.3	595	13 Q92124	Q92124 xenopus lae
28	442	18.2	694	13 Q91870	Q91870 xenopus lae
29	441.5	18.2	470	5 Q9NL15	Q9NL15 branchiosto
30	441	18.2	487	5 Q9NL13	Q9NL13 branchiosto
31	441	18.2	597	13 Q91871	Q91871 xenopus lae
32	440	18.2	579	11 Q9JU07	Q9JU07 mus musculus
33	438	18.1	1998	11 Q8CIW2	Q8CIW2 mus musculus
34	437	18.0	461	13 Q7ZW16	Q7ZW16 brachydanio
35	433	17.9	1102	11 Q80VN7	Q80VN7 mus musculus
36	432.5	17.8	426	11 Q55082	Q55082 mus musculus
37	431.5	17.8	473	13 Q9NL05	Q9NL05 eptatretus
38	431	17.8	398	4 Q9Y406	Q9Y406 homo sapien
39	430	17.7	274	11 Q9CWM8	Q9CWM8 rattus norv
40	429	17.7	433	13 Q9PT91	Q9PT91 brachydanio
41	429	17.7	433	13 Q7SYN6	Q7SYN6 brachydanio
42	428	17.7	589	5 Q8MM81	Q8MM81 caenorhabdi
43	428	17.7	593	11 Q7TSK0	Q7TSK0 mus musculus
44	428	17.7	624	5 Q9U3N7	Q9U3N7 caenorhabdi
45	428	17.7	1056	13 Q8AV93	Q8AV93 petromyzon

ALIGNMENTS

RESULT 1

Q61152	PRELIMINARY;	PRT;	453 AA.
ID	Q61152	PRELIMINARY;	PRT; 453 AA.
AC	Q61152; Q62404;		
DT	01-NOV-1998 (TrEMBLrel. 08, Created)		
DT	01-NOV-1998 (TrEMBLrel. 08, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Protein-tyrosine phosphatase 18 (EC 3.1.3.48) (PTP-K1) (fetal liver phosphatase 1) (FLP1) (PTP 49) (PTP HSCF).		
GN	PPN18 OR PTPK1.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=EMBRYO;		
RX	MEDLINE=96329547; PubMed=8695832;		
RA	Cheng J., Daimaru L., Fennie C., Lasky L.A.;		
RT	"A novel protein tyrosine phosphatase expressed in lin(10)CD34(hi)Scs(hi) hematopoietic progenitor cells.";		
RL	Blood 88:1156-1167(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=KIDNEY;		
RX	MEDLINE=97030045; PubMed=8875997;		
RA	Huang K., Schmers C.L., Grinberg A., Kozak C.A., Love P.E.;		
RT	"Cloning and characterization of PTP-K1, a novel nonreceptor protein tyrosine phosphatase highly expressed in bone marrow.";		
RL	Oncogene 13:1567-1573(1996).		
RN	[3]		
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.		
RC	STRAIN=C57BL/6; TISSUE=FETAL LIVER;		
RX	MEDLINE=97131769; PubMed=8977243;		
RA	Dosil M., Leiman N., Lemischka I.R.;		
RT	"Cloning and characterization of fetal liver phosphatase 1, a nuclear protein tyrosine phosphatase isolated from hematopoietic stem cells.";		
RL	Blood 88:4510-4525(1996).		
CC	-!- FUNCTION: MAY BE INVOLVED IN GROWTH AND DIFFERENTIATION OF		

RESULT 4
Q8TA96 PRELIMINARY; PRT; 372 AA.
AC Q8TA96;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Similar to protein tyrosine phosphatase, non-receptor type 18
DE (Brain-derived) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP STRAUSBERG R.;
RC TISSUS=Lymph, and Lymphoma;
RA Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC024280; AAH41562.1; -
DR EMBL; BC041562; AAH41562.1; -
DR GO; GO:0014787; F-hydrolase activity; IEA.
DR GO; GO:0004725; F-protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004872; F-receptor activity; IEA.
DR GO; GO:0006470; P-protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; ERTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase; Receptor.
FT NON TER 1
SQ SEQUENCE 372 AA; 47078 MW; 417CA80AA054CF8B CRC64;

Query Match 73.2%; Score 1775.5; DB 4; Length 372;
Best Local Similarity 76.2%; Pred. No. 9.3e-138;
Matches 349; Conservative 0; Mismatches 2; Indels 107; Gaps 1;

QY 1 MSRLDSARSFLERLEARGREGAVLAGFSDIQACSAANKADGVCSTVAGSRPENVRKN 60
DB 22 MSRLDSARSFLERLEARGREGAVLAGFSDIQACSAANKADGVCSTVAGSRPENVRKN 52
QY 61 RYKDVLPYDQTRVILSLQEGHSDYINGNFIKRGVDSGLAYIATQGLPHTLLDFWRLVW 120
DB 53 ----- 52
QY 121 EFGVKVILMACREIENGRCERYWAQEPLOTGLFCITLKEKWLNEDIMRLTKVTF 180
DB 53 -----KRCERYWAQEPLOTGLFCITLKEKWLNEDIMRLTKVTF 94
QY 181 QKESRSVYQLOQMSWPDGRGVPSSPDHMLANVEEARLQSGPEPLCVHCSAGCGRTGVLC 240
DB 95 QKESRSVYQLOQMSWPDGRGVPSSPDHMLANVEEARLQSGPEPLCVHCSAGCGRTGVLC 154
QY 241 TVDYVRQLLLTQMIIPDFSLFDVILKMRKQRPAAVQTEEQRYFLYHTVAQMFCSLTQNAS 300
DB 155 TVDYVRQLLLTQMIIPDFSLFDVILKMRKQRPAAVQTEEQRYFLYHTVAQMFCSLTQNAS 214
QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAI PRPPGGVLRISIVPGSPGHAMADTYAEQKR 360
DB 215 PHYQNIKENCAPLYDDALFLRTPQALLAI PRPPGGVLRISIVPGSPGHAMADTYAEQKR 274

RESULT 3
Q7Z637 PRELIMINARY; PRT; 351 AA.
AC Q7Z637;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE PTPN18 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RP STRAUSBERG R.;
RC TISSUS=Lymph;
RA MEDLINE=22388257; PubMed=12477932;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC052800; AAH52800.1; -
DR EMBL; BC052800; AAH52800.1; -
DR SFE99B48C5D0667C4 CRC64;

Query Match 73.2%; Score 1775.5; DB 4; Length 351;
Best Local Similarity 76.2%; Pred. No. 8.6e-138;
Matches 349; Conservative 0; Mismatches 2; Indels 107; Gaps 1;

QY 1 MSRLDSARSFLERLEARGREGAVLAGFSDIQACSAANKADGVCSTVAGSRPENVRKN 60
DB 1 MSRLDSARSFLERLEARGREGAVLAGFSDIQACSAANKADGVCSTVAGSRPENVRKN 31
QY 61 RYKDVLPYDQTRVILSLQEGHSDYINGNFIKRGVDSGLAYIATQGLPHTLLDFWRLVW 120
DB 32 ----- 31
QY 121 EFGVKVILMACREIENGRCERYWAQEPLOTGLFCITLKEKWLNEDIMRLTKVTF 180
DB 32 -----KRCERYWAQEPLOTGLFCITLKEKWLNEDIMRLTKVTF 73
QY 181 QKESRSVYQLOQMSWPDGRGVPSSPDHMLANVEEARLQSGPEPLCVHCSAGCGRTGVLC 240
DB 74 QKESRSVYQLOQMSWPDGRGVPSSPDHMLANVEEARLQSGPEPLCVHCSAGCGRTGVLC 133
QY 241 TVDYVRQLLLTQMIIPDFSLFDVILKMRKQRPAAVQTEEQRYFLYHTVAQMFCSLTQNAS 300
DB 134 TVDYVRQLLLTQMIIPDFSLFDVILKMRKQRPAAVQTEEQRYFLYHTVAQMFCSLTQNAS 193
QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAI PRPPGGVLRISIVPGSPGHAMADTYAEQKR 360
DB 194 PHYQNIKENCAPLYDDALFLRTPQALLAI PRPPGGVLRISIVPGSPGHAMADTYAEQKR 253

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QY 361 GAPAGAGSGTGTGTGARSAAEAPLYSKVTTPRAQRPQGAHAEDARGTLPGRVPAQSPAG 420
DB 275 GAPAGAGSGTGTGTGARSAAEAPLYSKVTTPRAQRPQGAHAEDARGTLPGRVPAQSPAG 334
QY 421 SGAYEDVAGGAQTGGGLGNLRIGRPGKPRDPPAEWTRV 458
DB 335 SGAYEDVAGGAQTGGGLGNLRIGRPGKPRDPPAEWTRV 372

RESULT 5
P70602
ID P70602 PRELIMINARY; PRT; 453 AA.
AC P70602;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE Protein tyrosine phosphatase 20.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=97067206; PubMed=8910608;
RA Aoki N., Yamaguchi-Aoki Y., Ullrich A.;
RT "The novel protein-tyrosine phosphatase PTP20 is a positive regulator
of PC12 cell neuronal differentiation.";
RL J. Biol. Chem. 271:29422-29426 (1996).
RN [2]
SEQUENCE FROM N.A.
RA Aoki N., Yamaguchi-Aoki Y., Ullrich A.;
RL Submitted (SPP-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U69673; AAC52896.1;
DR HSSP; Q06124; 2SHP.
DR GO; GO:0004725; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS00056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS00055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 453 AA; 50106 MW; 6CCCI32206FB69AE CRC64;

Query Match 72.4%; Score 1754.5; DB 11; Length 453;
Best Local Similarity 74.5%; Pred. No. 6.5e-136;
Matches 342; Conservative 37; Mismatches 73; Indels 7; Gaps 3;

QY 1 MSRLDARSFLERLEARGREGAVLAGEFSDIQACSAANKADGVCSVAGSPENVRKY 60
DB 1 MSRQSLVRSFLEQAEARDHRKGAILEAFSDIKARSAVKTEGVCSVAGSQGSKCN 60

QY 61 RYKDVLPYDQTRVLSLLQEGHSDYINGNFIKRVGDSGLAYIATQGPLHTLLDFWRLVW 120
DB 61 RYKDVLPYDQTRVLSLLQEGHSDYINGNFIKRVGDSGLAYIATQGPLHTLLDFWRLVW 120

QY 121 EFGVKVILMACRETLNCRKCRWAOEPIQTGLFCITLKEKWLNEIMRLTKVTF 180
DB 121 EFGVKVILMACRETLNCRKCRWAOEPIQTGLFCITLKEKWLNEIMRLTKVTF 180

QY 181 QKESRSYVQLQYMSWPDGRVPSPPDHMLAMVEEARLQSGSPFLCHVCSAGCGRTGVLC 240
DB 181 QKESRSYVQLQYMSWPDGRVPSPPDHMLAMVEEARLQSGSPFLCHVCSAGCGRTGVLC 240

QY 241 TVDVVROLLLTOMTPPDSFLDVLVLMKRPKORPAVQTEBOYRLYITVAMFCSTLONAS 300
DB 241 ADVIVRQLLLTQTPPDSFLDVLVLMKRPKORPAVQTEBOYRLYITVAMFCSTLONAS 300

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QY 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPVGGVLRISISVPGSPGHAMADTYAEQKR 360
DB 301 PHYQNIKENCAPLYDDALFLRTPQALLAIPRPVGGVLRISISVPGSPGHAMADTYAEQKR 360
QY 361 GAPAGAGSGTGTGTGARSAAEAPLYSKVTTPRAQRPQGAHAEDARGTLPGRVPAQSPAG 419
DB 361 GA-----SGS-TGPGTRADNPSTDTIYISQVAPRIQRPVSHSTENAGTTALGRVPADENPS 414
QY 420 GSCAYEDVAGGAQTGGGLGNLRIGRPGKPRDPPAEWTRV 458
DB 415 GPDAYEEVTDGAQTGGGLGNLRIGRPGKPRDPPAEWTRV 453

RESULT 6
Q7TMP9
ID Q7TMP9 PRELIMINARY; PRT; 802 AA.
AC Q7TMP9;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 8.
DE Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RX STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Utsdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055377; AAH5377.1; -.
KW Receptor.
SQ SEQUENCE 802 AA; 89694 MW; BB8C3AA618B28561 CRC64;

Query Match 30.9%; Score 749.5; DB 11; Length 802;
Best Local Similarity 43.7%; Pred. No. 7.3e-53;
Matches 160; Conservative 55; Mismatches 120; Indels 31; Gaps 7;

QY 27 AGEFSDIQACSAANKADGVCSVAGSPENVRKYKDVLPYDQTRVLSLLQEGHSDY 86
DB 25 ASEFLKLRQSKTKYKQIYPTTVAQRPQNIKKYKQIDILFYHSLVELSLTSDSDSS 84

QY 87 INGNFIRGVDSGLAYIATQGPLHTLLDFWRLVWFGVKVILMACRETLNCRKCRWAOE 146
DB 85 INASFIQGVYGFKAYIATQGPLSTLLDFWRLVWYEWYILVIVMACMEFEFGKKCEHYA 144

QY 147 QEQE-PIQTGLFCITLKEKWLNEIMRLTKVTFQKESRSYVQLQYMSWPDGRVPSPP 205
DB 145 EPGETQLQGFSPFSCEAEK-KKSDYKIRTLKAKFNNEITRIYQHYKNWPDHDPSSID 203

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QY 206 HMLAMVEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVYRQLLLTQMIPDPSLFDVWL 265
DB 204 PILELIWDMRCYQEDDCVPCIHCSAGCGRTGVCADVTWMLLKDGIIIPNFSVFNLIQ 263
QY 266 KMKORPAAVQTEQYFLYHTVAQMFCSLQNASPHYQNIKENCAPLYDDALFLRTPOA 325
DB 264 EMRTQPSLVQEQYELVYSAVLELF-----KRMVDVSNHLG-----REIQ 308
QY 326 LLATPRPGVLRISVPGS-----GHAMAD--TYAEQKRGAPAGAGSGTGTGTG 377
DB 309 QCSLPE-----QSLTEADSCPLDLPNARMVKTNNQSHSKQGAEBSTGGSLGLRTS 362
QY 378 ARSAAA 383
DB 363 TMNAEE 368
RESULT 7
Q9P0U2 PRELIMINARY; PRT; 799 AA.
AC Q9P0U2;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)
DE Protein tyrosine phosphatase.
GN PTP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal gland;
RA Huang C., Zhang C., Wu T., Peng Y., Gu Y., Zhang L., Jiang C., Li Y.,
RA Han Z., Wang Y., Chen Z., Fu G.;
RT "A novel gene expressed in human adrenal gland."
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF150732; AAF67472.1; -.
DR HSHP; P29350; IGWZ.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 799 AA; 90610 MW; 93F5385016F33D0C CRC64;
Query Match 30.0%; Score 726.5; DB 4; Length 799;
Best Local Similarity 46.9%; Pred. No. 5.7e-51;
Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;
QY 27 AGEFSDIOACSAANKADGVCSTVAGSRPENVRKRYKDVLPDQTRVILSLQEGHSDY 86
DB 25 ANEFLKLRQSTKYKADKTYPTTVAEKPKIKQRYKDIILPYDSRVLSLSITSDSSY 84
QY 87 INGNFIRGDSGLAVIATQGPLPHTLLDFWLVWFGVKVILMACREIENGKRCERYWA 146
DB 85 INANFIKVGYPEAVIATQGPLSTLLDFWNIWHSYLLIIVMACMEYENGKRCERYWA 144
QY 147 QEQE-PLQTGLFCITLIKEMLNEDIMLRTLVKTFQKESRSVYQYQVMSWDVGVPSPD 205
DB 145 EPGEMQLEFGPPSVSCEAEK-RKSDYIIRTLKVFNSERTIYQPHYKNWDPHDVPSID 203
QY 206 HMLAMVEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVYRQLLLTQMIPDPSLFDVWL 265
DB 204 PILELIWDMRCYQEDDCVPCIHCSAGCGRTGVCADVTWMLLKDGIIIPNFSVFNLIQ 263

QY 266 KMKORPAAVQTEQYFLYHTVAQMFCSLQNASPHYQNIKENCAP 312
DB 264 EMRTQPSLVQEQYELVYSAVLELFKQMDVIRDKHSGTESQAKHCIP 313
RESULT 8
Q86XU4 PRELIMINARY; PRT; 872 AA.
ID Q86XU4;
AC Q86XU4;
DT 01-JUN-2003 (TremBLrel. 24, Created)
DT 01-JUN-2003 (TremBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Protein tyrosine phosphatase, non-receptor type 12 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC050008; AAH50008.1; -.
DR GO; GO:0004725; P:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0004872; P:receptor activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003595; PTPC_motif.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; Tyr_PP.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PRTYPHPTASE.
DR SMART; SM00194; PTPC; 1.
DR SMART; SM00404; PTPC_motif; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
DR PROSITE; PS0056; TYR_PHOSPHATASE_2; 1.
DR PROSITE; PS0055; TYR_PHOSPHATASE_PTP; 1.
KW Receptor.
FT NON_TER.
SQ SEQUENCE 872 AA; 97952 MW; 84621458356585D4 CRC64;
Query Match 29.2%; Score 709; DB 4; Length 872;
Best Local Similarity 40.7%; Pred. No. 1.8e-49;
Matches 143; Conservative 66; Mismatches 116; Indels 26; Gaps 7;
QY 9 RSFLERLEA-----RCGREGAVLAGEFSDIOACSAANKADGVCSTVAGSRPENVRKRYK 63
DB 100 RKFQIRQVAMKSPDHNGEDN--FARDFMLRLSLTKYRTEKIYPTATGKEENVKKNRYK 157
QY 64 DVLVPDQTRVILSLQEGHSDYINGNFIRGDSGLAVIATQGPLPHTLLDFWLVWFG 123
DB 158 DILPFDHSVKLTLTPTSDSDYINANFIKVGYPKAYVATQGPLANTVIDFWRMIWEYN 217
QY 124 VKVILMACREIENGKRCERYM-AQEQLQTLGFCITLIKEMLNEDIMLRTLVKTFQK 182
DB 218 VVIIVNACREFEFMGRKKERYWPLYGEDPITFAPFKIS-CEDEQARTDYFIETLLLEFQN 276
QY 183 ESRSVYQYQVMSWDVGVSPDPHMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCTV 242
DB 277 ESRLLQFHYVWPDHDVDFSSDFSLDMSLKRKYQEHEDVFICHCAGCGRTGAI 336
QY 243 DYVROLQLLTQMIPDPSLFDVWLKMKRKPAAVQTEQYFLYHTVAQMFCSLQNASPH 302
DB 337 DYTWNLLKAGKTPKEEFNVFNLIQEMRTQSHSAVQTKQYELVHRAIAQLFQQLQIYEIH 396
QY 303 YQNIKENCAPLYDDALFLRTPOALLAI-----PRPPGGVLRISVPG 344
DB 397 -----GAOKIADGVNNEINTEINMISSIBPEKQDPSPPKPPR---TRSLVEG 439
RESULT 9
Q80UM4 PRELIMINARY; PRT; 775 AA.
ID Q80UM4

AC Q80UM4;
 DT 01-JUN-2003 (TREMELrel. 24, Created)
 DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Similar to protein tyrosine phosphatase, non-receptor type 12.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Frange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalusz D.B., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RA Strausberg R.;
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC051980; AAH51980.1; -
 DR GO: GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0004872; P:receptor activity; IEA.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR003595; PTPC motif.
 DR InterPro: IPR000387; TYR phosphatase.
 DR InterPro: IPR000242; TYR_PP.
 DR Pfam: PF00102; Y_phosphatase; 1.
 DR PRINTS: PR00700; PTRYPHPTASE.
 DR SMART: SM00194; PTPC; 1.
 DR SMART: SM00404; PTPC motif; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE 1; 1.
 DR PROSITE: PS00056; TYR_PHOSPHATASE 2; 1.
 DR PROSITE: PS00055; TYR_PHOSPHATASE_Ptp; 1.
 KW Receptor.
 SQ SEQUENCE 775 AA; 86526 MW; EDIA7AS77CE4352C CRC64;
 Query Match 29.1%; Score 706; DB 11; Length 775;
 Best Local Similarity 25.1%; Pred. No. 2.7e-49;
 Matches 195; Conservative 83; Mismatches 162; Indels 336; Gaps 17;
 QY 9 RSFLERLEA-----RGREGAVLAGEFSDIQACSAANKADGVCSVAGSPENVKRYK 63
 DB 8 RRFQVRQAMKSPDHNGEDN--FARDFMRRLRSTKRTKIYPTATGEENKKNRYK 65
 QY 64 DVLFDYDQTRVLSLQBEHSDYINGNFIKVGDSGLAYIATQGPLHTLDFWRLVWEFG 123
 DB 66 DILFFDSRVLTKLTPTSDSYINANFNGVYGPAYVATQGPLANTVIDFWMIWEYN 125
 QY 124 VKVILMACREINERKRCERYW-AQOEPEQTGLFCITLKEKWLMDIWLRLKVTFOK 192
 DB 126 VVIIVMACREFEMGRKKCYRWLYGDDPTTFAPFKISCNEQ-ARTDYFIRTLLEFQN 194
 QY 183 ESRSVYQLQYMSWDRGVPSPPDHMLANVBEARRLQSGPEPLCVHCSAGCGTGVLCV 242
 DB 183 ESRRLYQHYVNVWPHDVPSSFDSDILMTSLMRKYQEHEDVFCIHCSAGCGRTGAICAI 244
 QY 243 DYVRQLLTQMIPDPFSDVVLKMKRKORPAAVQTEEOYRFLYHTVQWFCSTLQ----- 297
 DB 245 DTWNLLKAGKIPDEFNVNLIQEMRTQHSVAQVKEQVELVHRAIAQVFEKQLQLYEIH 304
 QY 298 ----- 297
 DB 305 GAKIADGNEITTTGTMVSSIDSEKQDPPKPPRTTRSCVLGEADAKEILQPPEHPVPPPI 364
 QY 298 -----NASP----- 301
 DB 365 LTFSPSPAPPTVTWQSDRHYKPVLMASPEQHPADLNRSYDKSADPMCKSESALIEH 424
 QY 302 -----HYQIKENCAFLYDDALFLRT--PQA 325
 DB 425 IDKLLERNLSFEIKVPLQEGPKSFDGNTLLNRGHAIIKKSASSSVWD-----RTSKPQE 479
 QY 326 ILA-----IPRP-----PGGVLRSI- 340
 DB 480 LSAGALKVDDVDSQNSCADSAHSHRAAESSESSQNSHTPPRPDCLPLDKKHGVTWSLH 539
 QY 341 -----SVPGSPGHAMADTY-----AEQKR----- 360
 DB 540 GPNATPVDPDSDGKSPDNHSQTLKTVSSTPNSTAEAEHDLTEHNSSPLLKAPLSFTN 599
 QY 361 -----CAPAGAGSGTGTGTGA-----RSAAEAPLYSKVTPR----- 393
 DB 600 PLHSDSDSDGSGSDGAVTRNKTSISTASATVSPASSAESACTRVLPMSTARQEVAGTP 659
 QY 394 ---AORPGAHADARGTLPGRV----- 413
 DB 660 HSGAEKDADVSESPPLPERTPESFVLADMPVREWEHLPNQEWSEQSEGLTTSQNE 719
 QY 414 -----ADQSPAGSGAYEDVA-GGAQTGGLGNLRIGRPKGRDPPPAEW 456
 DB 720 KHDAGGIHTASADSPPAFSDKKQDITKSPAEDVDIGFGNRCGKPKGPREPSEWT 775

RESULT 10

Q63745 ID Q63745 PRELIMINARY; PRT; 382 AA.
 AC Q63745;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Protein tyrosine phosphatase.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=95046282; PubMed=7957881;
 RA Moriyama T., Kawanishi S., Inoue T., Imai E., Kaneko T., Xia C.,
 RA Takenaka M., Kamada T., Ueda N.;
 RT "cDNA cloning of a cytosolic protein tyrosine phosphatase (RKTP) from
 RT rat kidney."
 RL FEBS Lett. 353:305-308 (1994).
 DR EMBL: D38072; BAA07266.1; -.
 DR PIR: S48748; S48748.
 DR HSSP: Q06124; 2SHP.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0004725; P:protein tyrosine phosphatase activity; IEA.
 DR GO: GO:0006470; P:protein amino acid dephosphorylation; IEA.
 DR InterPro: IPR000387; TYR phosphatase.
 DR InterPro: IPR000242; TYR_PP.
 DR Pfam: PF00102; Y_phosphatase; 1.
 DR PRINTS: PR00700; PTRYPHPTASE.
 DR SMART: SM00194; PTPC; 1.
 DR PROSITE: PS00383; TYR_PHOSPHATASE 1; 1.
 DR PROSITE: PS00056; TYR_PHOSPHATASE_2; 1.


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DR PROSITE; PS00383; TYR_PHOSPHATASE 1; FALSE_NEG.
DR PROSITE; PS00556; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
KW Signal.
FT SIGNAL.
FT CHAIN.
SQ SEQUENCE 1118 AA; 123038 MW; F73E3967ECE59F00 CRC64;

Query Match 20.3%; Score 491.5; DB 4; Length 1118;
Best Local Similarity 43.3%; Pred. No. 2e-31;
Matches 116; Conservative 36; Mismatches 91; Indels 25; Gaps 9;

QY 47 STVAGSRPENVRNRYKDVLPYDQTRVILSLLOEGHSDYINGNFIRGVDSGLAYIATQG 106
Db 837 SQMVASASENNAKRYRNVLVDWSRVPLKPIHEEPGSDYINASFMPGLMSPQEFATQG 896
QY 107 PLPHTLLDFWLVWVEFGVKVILMACRETEGKRCERYWAOEQPLQTGLFCITL----I 162
Db 897 PLPQTGVDFWLVWVEGQSHTLVMLTNCMEAGRVKCEHYWPLDSQFCTHGLRLVTLVGEEV 956
QY 163 KEKWLNEIMRLTKVTFQKESRSYVQYQVMSWPDGRGVPSPDHMLAMVEEARR-----L 217
Db 957 MENWTVRELL--LQVEEQK-TLSVRQFHYQAWPDHGVSPSPDTLLAFWRLQWLDQTM 1013
QY 218 QSGPEPLCVHCSAGCGRTGVLCTVD-YVRQLLTQMIPPPDFSLFDVVLKQKQRPAAVQ 276
Db 1014 EGGPP---IVHCSAGVGRGTGLIALDLLRLQLOSEGLLGP----FSFVRKQRESRPLMVQ 1066
QY 277 TEEQYRFLYHTVAOMFCSTLQNASPHYQ 304
Db 1067 TEAQYVFLH----QCICGS-SNSQPRFQ 1089

RESULT 15
Q9HD43
ID Q9HD43 PRELIMINARY; PRT; 1115 AA.
AC Q9HD43
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Transmembrane-type protein tyrosine phosphatase H.
GN PTPRH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21328879; PubMed=11435690;
RA Marieros A.G., Wehenni H., Reichenberger E., Antonarakis S.E.,
RA Kriegl T., Olsen B.R.;
RT "Gene for the human transmembrane-type protein tyrosine phosphatase H
RT (PTPRH): genomic structure, fine-mapping and its exclusion as a
RT candidate for Peutz-Jeghers syndrome."
RL Cytogenet. Cell Genet. 92:213-216(2001).
DR EMBL; AF275150; AAF91411.1; JOINED.
DR EMBL; AF275131; AAF91411.1; JOINED.
DR EMBL; AF275132; AAF91411.1; JOINED.
DR EMBL; AF275133; AAF91411.1; JOINED.
DR EMBL; AF275134; AAF91411.1; JOINED.
DR EMBL; AF275135; AAF91411.1; JOINED.
DR EMBL; AF275136; AAF91411.1; JOINED.
DR EMBL; AF275137; AAF91411.1; JOINED.
DR EMBL; AF275138; AAF91411.1; JOINED.
DR EMBL; AF275139; AAF91411.1; JOINED.
DR EMBL; AF275140; AAF91411.1; JOINED.
DR EMBL; AF275141; AAF91411.1; JOINED.
DR EMBL; AF275142; AAF91411.1; JOINED.
DR EMBL; AF275143; AAF91411.1; JOINED.
DR EMBL; AF275144; AAF91411.1; JOINED.
DR EMBL; AF275145; AAF91411.1; JOINED.
DR EMBL; AF275146; AAF91411.1; JOINED.
DR EMBL; AF275147; AAF91411.1; JOINED.

DR EMBL; AF275148; AAF91411.1; JOINED.
DR EMBL; AF275149; AAF91411.1; JOINED.
DR HSSP; P18052; IYFO.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004725; F:protein tyrosine phosphatase activity; IEA.
DR GO; GO:0006470; P:protein amino acid dephosphorylation; IEA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR008957; FN.III-like.
DR InterPro; IPR000387; TYR_phosphatase.
DR InterPro; IPR000242; TYR_PP.
DR Pfam; PF00041; fn3; 7.
DR Pfam; PF00102; Y_phosphatase; 1.
DR PRINTS; PR00700; PTPPHPTASE.
DR SMART; SM00060; FN3; 5.
DR SMART; SM00194; PTPC; 1.
DR PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.
DR PROSITE; PS00556; TYR_PHOSPHATASE 2; 1.
DR PROSITE; PS00555; TYR_PHOSPHATASE_PTP; 1.
KW Hydrolase.
SQ SEQUENCE 1115 AA; 122352 MW; A7A1AB24CFCD3846 CRC64;

Query Match 20.2%; Score 489.5; DB 4; Length 1115;
Best Local Similarity 40.8%; Pred. No. 2.9e-31;
Matches 116; Conservative 43; Mismatches 98; Indels 27; Gaps 9;

QY 47 STVAGSRPENVRNRYKDVLPYDQTRVILSLLOEGHSDYINGNFIRGVDSGLAYIATQG 106
Db 835 SQMVASASENNAKRYRNVLVDWSRVPLKPIHEEPGSDYINASFMPGLMSPQEFATQG 894
QY 107 PLPHTLLDFWLVWVEFGVKVILMACRETEGKRCERYWAOEQPLQTGLFCITL----I 162
Db 895 PLPQTGVDFWLVWVEGQSHTLVMLTNCMEAGRVKCEHYWPLDSQFCTHGLRLVTLVGEEV 954
QY 163 KEKWLNEIMRLTKVTFQKESRSYVQYQVMSWPDGRGVPSPDHMLAMVEEARR-----L 217
Db 955 MENWTVRELL--LQVEEQK-TLSVRQFHYQAWPDHGVSPSPDTLLAFWRLQWLDQTM 1011
QY 218 QSGPEPLCVHCSAGCGRTGVLCTVD-YVRQLLTQMIPPPDFSLFDVVLKQKQRPAAVQ 276
Db 1012 EGGPP---IVHCSAGVGRGTGLIALDLLRLQLOSEGLLGP----FSFVRKQRESRPLMVQ 1064
QY 277 TEEQYRFLYHTVAOMFCSTLQNASPH--YQNIK---ENCAPL 313
Db 1065 TEAQYVFLHQCILRFLQQAQAPAEKVEPYEDVENLIYENVAAI 1108

Search completed: August 17, 2004, 20:44:08.
Job time : 46 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 17, 2004, 20:28:43 ; Search time 54 Seconds
(without alignments)
2396.421 Million cell updates/sec

Title: US-10-087-993A-36

Perfect score: 2424

Sequence: 1 MSRLDSARSPLERARGG.....NLRIGRPGKPRDPAETRV 458

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2411	99.5	458	AAW49908	AAW49908 Human bra
2	1770.5	73.0	453	AAW37254	AAW37254 Novel non
3	1764.5	72.8	353	ADC99051	ADC99051 Human KPP
4	1754.5	72.4	453	AAW49906	AAW49906 Rat prote
5	830	34.2	155	AAW37255	AAW37255 Partial h
6	755.5	31.2	802	AAW28654	AAW28654 Murine Cy
7	727.5	30.0	807	AAW89247	AAW89247 Human tyr
8	726.5	30.0	799	AAW78623	AAW78623 Human tyr
9	710	29.3	773	ABW57374	ABW57374 Mouse isc
10	709	29.2	780	AAW67252	AAW67252 Human pro
11	709	29.2	780	ADC64343	ADC64343 FLJ20037.
12	708	29.2	692	AAW28653	AAW28653 Human Cyt
13	708	29.2	780	AAW51205	AAW51205 Human Cyt
14	708	29.2	808	AAW28652	AAW28652 Human Cyt
15	705	29.1	775	AAW67250	AAW67250 Mouse pro
16	700	28.9	780	AAW51201	AAW51201 Human PTP
17	699	28.8	780	AAW67253	AAW67253 Human mut
18	698	28.8	780	AAW51202	AAW51202 Human PTP
19	695	28.7	775	AAW67251	AAW67251 Murant mo
20	665	27.4	312	AAW78281	AAW78281 Human PTP
21	658	27.1	253	AAW59383	AAW59383 Human pro
22	529	21.8	237	ADC64297	ADC64297 Human SID
23	493.5	20.4	313	AAW78277	AAW78277 Human SAP
24	491.5	20.3	1093	ABR43689	ABR43689 Human tyr
25	491.5	20.3	1118	ABR43688	ABR43688 Human tyr

26	486.5	20.1	255	4	AAW59379	AAW59379 Human pro
27	485	20.0	1705	5	ABW52348	ABW52348 Protein r
28	474	19.6	1711	2	AAW70506	AAW70506 Osteotest
29	474	19.6	1711	5	ABW52349	ABW52349 Protein r
30	468	19.3	274	4	AAW59385	AAW59385 Protein c
31	467	19.3	595	2	AAW99312	AAW99312 Human SH-
32	464	19.1	1711	2	AAW70507	AAW70507 Mutant os
33	463.5	19.1	341	4	AAW78283	AAW78283 PT21. 12/
34	463.5	19.1	513	2	AAW99314	AAW99314 Rat M1PTP
35	463	19.1	593	2	AAW52991	AAW52991 Human pro
36	463	19.1	595	4	AAW59233	AAW59233 SHP-1 act
37	463	19.1	595	4	AAW59216	AAW59216 SHP-1 pro
38	463	19.1	595	4	AAW59239	AAW59239 SHP-1 E74
39	463	19.1	595	4	AAW59232	AAW59232 SHP-1 act
40	463	19.1	595	4	AAW59238	AAW59238 SHP-1 D59
41	463	19.1	597	3	AAW26873	AAW26873 Human Src
42	463	19.1	597	6	ABW59695	ABW59695 Human pro
43	463	19.1	621	3	AAW52289	AAW52289 Human HCP
44	463	19.1	621	5	ABW41954	ABW41954 Human ova
45	463	19.1	824	3	AAW52288	AAW52288 Human HCP

ALIGNMENTS

RESULT 1
AAW49908
ID AAW49908 standard; protein; 458 AA.
XX AAW49908;
AC AAW49908;
XX AAW49908;
DT 20-JUL-1998 (first entry)
XX Human brain derived phosphatase 1 (BDP-1).
XX Human brain derived phosphatase 1 (BDP-1).
KW Brain derived phosphatase 1; BDP-1; human; receptor;
KW protein tyrosine phosphatase; signal transduction; therapy; diagnosis.
XX Homo sapiens.
XX WO9748723-A2.
XX 24-DEC-1997.
XX 17-JUN-1997; 97WO-IB000946.
XX 17-JUN-1996; 96US-0019629P.
PR 09-AUG-1996; 96US-0023485P.
PR 13-NOV-1996; 96US-0030860P.
PR 15-NOV-1996; 96US-0030964P.
PR 19-DEC-1996; 96US-0034286P.
XX (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX Ullrich A, Kharitonov AI, Aoki N, Wang HY, Chen Z, Nayler O;
Kim YW;
WPI; 1998-120302/11.
DR N-PSDB; AAV17099.
XX New phosphatase and kinase enzyme(s) - useful in the diagnosis and
treatment of signal transduction disorders.
XX Claim 11; Fig 3a-d; 138pp; English.
XX This polypeptide comprises a novel human protein tyrosine phosphatase
(PTP), designated brain derived phosphatase 1 (BDP-1), that is expressed
in most tissues and cell lines at basal level, but expressed high in
epithelium origin cell lines and cancer cell lines. The amino acid
sequence was deduced from a cDNA clone (see AAV17099) isolated from a
haematopoietic MEG01 cDNA library. The invention relates to novel
proteins (see AAW49906-14) involved in cellular signal transduction and
to the nucleic acids (see AAV17097-99) coding for them, and provides

CC vectors, host cells, purified recombinant proteins, methods for
 CC identifying compounds that activate or inhibit the novel proteins, as
 CC well as methods for the diagnosis and treatment of diseases associated
 CC with the novel proteins
 XX Sequence 458 AA;
 SQ
 Query Match 99.5%; Score 2411; DB 2; Length 458;
 Best Local Similarity 99.8%; Pred. No. 1.3e-220;
 Matches 457; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MSRLDSARSFLERLEARGREGAVLAGEFSDIOACSAANKADGVCSTVAGSRPENVRKN 60
 DB 1 MSRLDSARSFLERLEARGREGAVLAGEFSDIOACSAANKADGVCSTVAGSRPENVRKN 60
 QY 61 RYKDVLPYDQTRVILSLQEGHSDYINGNFIKRGVDSGLAYIATQGPPLHTLLDFWRLVW 120
 DB 61 RYKDVLPYDQTRVILSLQEGHSDYINGNFIKRGVDSGLAYIATQGPPLHTLLDFWRLVW 120
 QY 121 EFGVKVILMACREIENGRCRCRYWAQOEPLQGLFCITILIKEKWLNEIMLTLLKVTFF 180
 DB 121 EFGVKVILMACREIENGRCRCRYWAQOEPLQGLFCITILIKEKWLNEIMLTLLKVTFF 180
 QY 161 OKESRSVYQLOVMSWPDGRGVSSPDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVLG 240
 DB 161 OKESRSVYQLOVMSWPDGRGVSSPDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVLG 240
 QY 241 TVDYVRQLLLTQMIIPDFSLFDVLMKMRKQRPAAVQTEEQYRFLYHTVAQMFCSLTQNAS 300
 DB 241 TVDYVRQLLLTQMIIPDFSLFDVLMKMRKQRPAAVQTEEQYRFLYHTVAQMFCSLTQNAS 300
 QY 301 PHYONIKENCAPLYDDALFLRTPQALLAI PRPPGCVLESISVPGSPGHAMADTYAEQKR 360
 DB 301 PHYONIKENCAPLYDDALFLRTPQALLAI PRPPGCVLESISVPGSPGHAMADTYAEQKR 360
 QY 361 GAPAGAGSGTGTTGTGARSABEAPLYSKVTPRAQRPAGHAEDARGTLPGKVPADQSPAG 420
 DB 361 GAPAGAGSGTGTTGTGARSABEAPLYSKVTPRAQRPAGHAEDARGTLPGKVPADQSPAG 420
 QY 421 SGAYEDVAGGAQTGGLGNLRIKGRPKGRDPPAEWTRV 458
 DB 421 SGAYEDVAGGAQTGGLGNLRIKGRPKGRDPPAEWTRV 458
 RESULT 2
 AAW37254
 ID AAW37254 standard; protein; 453 AA.
 XX
 AC AAW37254;
 DT 09-APR-1998 (first entry)
 XX
 DE Novel non-receptor tyrosine phosphatase of hematopoietic stem cells.
 KW Non-receptor protein tyrosine phosphatase; hematopoietic stem cell;
 XW PTP HSC; progenitor cell; tyrosine phosphatase domain; PTP HSC agonist;
 KW tyrosine dephosphorylation; tyrosine phosphatase; PTP HSC antagonist;
 XX stem cell differentiation.
 OS Mus sp.
 XX
 FT Key Location/Qualifiers
 FT Domain 6..303
 FT /note= "tyrosine phosphatase domain"
 FT Active-site 37
 FT /note= "phosphorylated by protein kinases A and C; also appears to negatively regulate PTPase activity"
 FT Active-site 229
 FT /note= "active site cysteine residue"
 FT Region 312..428
 FT /note= "pro, Ser and Thr rich region"
 FT Region 430..450
 FT /note= "homologous to a nuclear localization signal found

FT on murine PTP PEP"
 XX WO9735019-A1.
 XX 25-SEP-1997.
 XX 17-MAR-1997; 97WO-US005278.
 XX 22-MAR-1996; 96US-00620526.
 XX (GETH) GENENTECH INC.
 XX Lasky LA, Cheng J;
 XX WPI; 1997-480224/44.
 XX N-PSDB; AAV03112.
 XX Haematopoietic stem cell non-receptor protein tyrosine phosphatase -
 XX useful for expansion of undifferentiated stem cells in cell culture.
 XX Claim 9; Fig 1; 66pp; English.
 XX
 CC The present sequence represents a novel murine non-receptor protein
 CC tyrosine phosphatase of hematopoietic stem cells (PTP HSC). This protein
 CC is predominantly expressed in early hematopoietic stem cells (HSCs) or
 CC progenitor cells, and lacks expression in adult tissues. The protein has
 CC a N-terminal tyrosine phosphatase domain, followed by a region rich in
 CC serine, threonine and proline and a C-terminal region of about 15-25
 CC amino acids which is rich in basic amino acid residues. The protein is
 CC capable of tyrosine dephosphorylation in hematopoietic progenitor cells,
 CC and functional derivatives of such native tyrosine phosphatases. The
 CC phosphatase domain of the PTP HSC or a PTP HSC-expressing HSC or
 CC progenitor cell can be used in an assay for the identification of PTP HSC
 CC antagonists or agonists. The antagonist can be used to induce the
 CC differentiation of stem cells, such as undifferentiated malignant
 CC hematopoietic cells, e.g. leukaemia cells, which may facilitate their
 CC treatment. The PTP HSC or an agonist antibody against the PTP HSC can be
 CC used for the expansion of undifferentiated stem cells in cell culture
 CC (this allows expansion of HSC prior to autologous or heterologous bone
 CC marrow transplantation), while the agonist antibody along with a
 CC hematopoietic growth factor can be used for the expansion of
 CC undifferentiated stem cells in vivo
 XX Sequence 453 AA;
 SQ
 Query Match 73.0%; Score 1770.5; DB 2; Length 453;
 Best Local Similarity 74.7%; Pred. No. 1.4e-159;
 Matches 343; Conservative 32; Mismatches 77; Indels 7; Gaps 2;
 QY 1 MSRLDSARSFLERLEARGREGAVLAGEFSDIOACSAANKADGVCSTVAGSRPENVRKN 60
 DB 1 MSRLDSARSFLERLEARGREGAVLAGEFSDIOACSAANKADGVCSTVAGSRPENVRKN 60
 QY 61 RYKDVLPYDQTRVILSLQEGHSDYINGNFIKRGVDSGLAYIATQGPPLHTLLDFWRLVW 120
 DB 61 RYKDVLPYDQTRVILSLQEGHSDYINGNFIKRGVDSGLAYIATQGPPLHTLLDFWRLVW 120
 QY 121 EFGVKVILMACREIENGRCRCRYWAQOEPLQGLFCITILIKEKWLNEIMLTLLKVTFF 180
 DB 121 EFGVKVILMACREIENGRCRCRYWAQOEPLQGLFCITILIKEKWLNEIMLTLLKVTFF 180
 QY 161 OKESRSVYQLOVMSWPDGRGVSSPDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVLG 240
 DB 161 OKESRSVYQLOVMSWPDGRGVSSPDHMLAMVEEARLQSGGPEPLCVHCSAGCGRTGVLG 240
 QY 241 TVDYVRQLLLTQMIIPDFSLFDVLMKMRKQRPAAVQTEEQYRFLYHTVAQMFCSLTQNAS 300
 DB 241 TVDYVRQLLLTQMIIPDFSLFDVLMKMRKQRPAAVQTEEQYRFLYHTVAQMFCSLTQNAS 300
 QY 301 PHYONIKENCAPLYDDALFLRTPQALLAI PRPPGCVLESISVPGSPGHAMADTYAEQKR 360
 DB 301 PHYONIKENCAPLYDDALFLRTPQALLAI PRPPGCVLESISVPGSPGHAMADTYAEQKR 360

QY 361 GAPAGAGSGTGTGTGARSAAEAPLYSKVTPRAORPGAHAEADARGTLP-CRVPADQSPA 419
 DB 361 GASAGTGPGPAPST-----DPIYSQVAPRAQRPVHAHTEDAQGTALRRVPADQNSS 414
 QY 420 GSGAYEDVAGGAQTGGGLGFNLRIKRPKGRDPPPAEWTRV 458
 DB 415 GPDAYEEVTDGAQTGGGLGFNLRIKRPKGRDPPPAEWTRV 453

RESULT 3
 ADC99051
 ID ADC99051 standard; protein; 353 AA.

AC ADC99051;
 DT 01-JAN-2004 (first entry)
 XX Human KPP protein - SEQ ID 4.
 DE
 XX anti-HIV; anti-allergic; anti-inflammatory; antianaemic; antiparkinsonian;
 KW nootropic; anticonvulsant; antiarteriosclerotic; antiasthmatic;
 KW immunosuppressive; antithyroid; cytostatic; hepatotropic; dermatological;
 KW antidiabetic; nephrotropic; antitumor; thyrominetic; neuroprotective;
 KW osteopathic; antichronic; antiparasitic; antihelminthic; antiparasitic;
 KW uropathic; ophthalmological; antirheumatic; haemostatic; antibacterial;
 KW virucide; protozoacide; fungicide; kinase; phosphatase; cirrhosis; hepatitis;
 KW cell proliferative disorder; atherosclerosis; cirrhosis; hepatitis;
 KW cancer; developmental; mental retardation; neurological;
 KW Alzheimer's disease; Parkinson's; autoimmune; inflammatory; Crohn's;
 KW diabetes mellitus; viral; bacterial; fungal; parasitic; protozoan;
 KW helminthic infection; transgenic; gene therapy; human; enzyme.

OS Homo sapiens.
 XX
 XX WO2003033680-A2.
 XX 24-APR-2003.
 XX 17-OCT-2002; 2002WO-US033723.
 XX 19-OCT-2001; 2001US-0345474P.
 PR 02-NOV-2001; 2001US-0343910P.
 PR 13-NOV-2001; 2001US-0333098P.
 PR 16-NOV-2001; 2001US-0332424P.
 PR 30-NOV-2001; 2001US-0334288P.

(INCY-) INCYTE GENOMICS INC.
 XX Bandman O, Baughn MR, Becha SD, Borowsky ML, Duggan BM;
 PI Emerling BM, Forsythe IJ, Gandhi AR, Gorvad AE, Griffin JA;
 PI Gururajan K, Haralia AFA, Khan FA, Lal FG, Lee EA, Lee SY;
 PI Lindquist EA, Lu DAM, Lu Y, Marquis JP, Nguyen DB, Arvizu CS;
 PI Ramkumar J, Recipon SA, Richardson TW, Swarnakar A, Tang YT;
 PI Thornton MB, Tran UK, Chawla NK, Warren BA, Yang J, Yao MG, Yue H;
 PI Zebarjadian Y;
 XX WPI. 2003-403214/38.
 DR N-PSDB; ADC99103.

XX New human kinases and phosphatases and polynucleotides, useful for
 PT diagnosing, treating or preventing autoimmune or inflammatory disorders
 PT (e.g. AIDS, allergy or anemia), multiple sclerosis, osteoarthritis,
 PT cancer or hepatitis.
 XX Claim 1; SEQ ID NO 4; 424pp; English.
 PS
 XX The invention relates to a novel isolated polypeptide which is a human
 CC kinase and phosphatase (KPP). The KPP polypeptides, polynucleotides,
 CC agonists and antagonists are useful for diagnosing, treating or
 CC preventing cell proliferative disorders such as atherosclerosis,
 CC cirrhosis, hepatitis and cancer, developmental disorders e.g. mental
 CC retardation, neurological disorders including Alzheimer's disease and
 CC Parkinson's disease, autoimmune and inflammatory disorders such as

CC Crohn's disease and diabetes mellitus and finally, viral, bacterial,
 CC fungal, parasitic, protozoan or helminthic infections. Furthermore, the
 CC polynucleotides encoding KPP may be useful for creating transgenic
 CC animals to model human disease, as well as during gene therapy
 CC procedures. The current sequence is that of the human KPP protein of the
 CC invention.
 XX
 SQ Sequence 353 AA;

Query Match 72.8%; Score 1764.5; DB 7; Length 353;
 Best Local Similarity 75.9%; Pred. No. 3.7e-159;
 Matches 349; Conservative 0; Mismatches 2; Indels 109; Gaps 2;

QY 1 MSRLSDARSFLERLEARGREGAVLAGEFSDIQAASAAWKGVCSTVAGSRPENVRKN 60
 DB 1 MSRLSDARSFLERLEARGREGAVLAGEFSDIQAASAAWKGVCSTVAGSRPENVRKN 31
 QY 61 RYKDVLPYDQTRVILSLLOEBSHSDYINGNFIRGVDGSLAYIATOGPLPHILLDFWRLVW 120
 DB 32 ----- 31
 QY 121 EFGVKVILMACREIENGKRCERYWAQEQPLQTGLFCITLIKELKWLNEIDIMRLTKVTF 180
 DB 32 -----KRCERYWAQEQPLQTGLFCITLIKELKWLNEIDIMRLTKVTF 73
 QY 181 QKESRVSVOQYMSWPDGVPSPDHMLAMVEARLQSGPEPLCVHCSACCGRTGVLC 240
 DB 74 QKESRVSVOQYMSWPDGVPSPDHMLAMVEARLQSGPEPLCVHCSACCGRTGVLC 133
 QY 241 TVDYVRQLLTQMIIPDFSLFDVVKORQKORAAVQTEBOYRFLYHTVAQMFCSLTQNAS 300
 DB 134 TVDYVRQLLTQMIIPDFSLFDVVKORQKORAAVQTEBOYRFLYHTVAQMFCSLTQNAS 193
 QY 301 PHYQNIKENCAPLYDDALFLRTPOALLAIPRPPGGVLSISVPGSPGHAMADTYAEQKR 360
 DB 194 PHYQNIKENCAPLYDDALFLRTPOALLAIPRPPGGVLSISVPGSPGHAMADTYAVVQKR 253
 QY 361 GAPAGAGSGTQ--TGTCGARSAAEAPLYSKVTPRAORPGAHAEADARGTLPGRVPADQSP 418
 DB 254 GAPAGAGSGTQGTGTGTCGARSAAEAPLYSKVTPRAORPGAHAEADARGTLPGRVPADQSP 313
 QY 419 AGSGAYEDVAGGAQTGGGLGFNLRIKRPKGRDPPPAEWTRV 458
 DB 314 AGSGAYEDVAGGAQTGGGLGFNLRIKRPKGRDPPPAEWTRV 353

RESULT 4
 AAW49906
 ID AAW49906 standard; protein; 453 AA.
 AC AAW49906;
 XX 20-JUL-1998 (first entry)
 DE Rat protein tyrosine phosphatase PRP20.
 KW Protein tyrosine phosphatase; PTP20; rat; signal transduction;
 KW cell differentiation; cancer; neural injury; therapy.
 XX Rattus sp.
 XX WO9748723-A2.
 XX 24-DEC-1997.
 XX 17-JUN-1997; 97WO-IB000946.
 XX 17-JUN-1996; 96US-0019629P.
 PR 09-AUG-1996; 96US-0023485P.
 PR 13-NOV-1996; 96US-0030860P.
 PR 15-NOV-1996; 96US-0030964P.
 PR 19-DEC-1996; 96US-0034286P.

RESULT 6

AY28654	standard; protein; 802 AA.	AY28654	standard; protein; 802 AA.
AY28654	(first entry)	AY28654	(first entry)
01-OCT-1999		01-OCT-1999	
Murine Cytoplasmic phosphatase, Z70PEP protein.		Murine Cytoplasmic phosphatase, Z70PEP protein.	
Lymphoid Protein Tyrosine Phosphatase; Lyp protein; lymphoid cell; intracellular tyrosine phosphatase; PTPase; lymphocyte; murine; protein tyrosine kinase; PRKs; immunosuppressant; PEST sequence; T cell antigen receptor signalling; autoimmune disease; transplant; cytokine receptor signalling.		Lymphoid Protein Tyrosine Phosphatase; Lyp protein; lymphoid cell; intracellular tyrosine phosphatase; PTPase; lymphocyte; murine; protein tyrosine kinase; PRKs; immunosuppressant; PEST sequence; T cell antigen receptor signalling; autoimmune disease; transplant; cytokine receptor signalling.	
Mus sp.		Mus sp.	
Key	Location/Qualifiers	Key	Location/Qualifiers
Domain	27..288	Domain	27..288
	/label= PTPase domain		/label= PTPase domain
	/note= "Catalytic protein tyrosine phosphatase domain"		/note= "Catalytic protein tyrosine phosphatase domain"
Binding-site	613..621	Binding-site	613..621
	/label= SH3 binding site		/label= SH3 binding site
	/note= "proline rich sequence"		/note= "proline rich sequence"
Binding-site	689..695	Binding-site	689..695
	/label= SH3 binding site		/label= SH3 binding site
	/note= "proline rich sequence"		/note= "proline rich sequence"
Binding-site	790..798	Binding-site	790..798
	/label= SH3 binding site		/label= SH3 binding site
	/note= "proline rich sequence"		/note= "proline rich sequence"
WO9936548-A1.		WO9936548-A1.	
22-JUL-1999.		22-JUL-1999.	
18-JAN-1999;	99WO-CA000038.	18-JAN-1999;	99WO-CA000038.
16-JAN-1998;	98CA-02220853.	16-JAN-1998;	98CA-02220853.
(HSCR-) HSC RES & DEV LP.		(HSCR-) HSC RES & DEV LP.	
Roifman CM;		Roifman CM;	
WPI; 1999-444404/37.		WPI; 1999-444404/37.	
New nucleic acid encoding intracellular tyrosine phosphatase and related proteins, used to modulate signaling through T cells, particularly as immunosuppressant.		New nucleic acid encoding intracellular tyrosine phosphatase and related proteins, used to modulate signaling through T cells, particularly as immunosuppressant.	
Disclosure; Page 63-64; 105pp; English.		Disclosure; Page 63-64; 105pp; English.	
The present protein sequence is that of the murine phosphatase, Z70PEP that has a single catalytic domain. The non-catalytic portion of the phosphatase contains unique sequences, including five PEST sequences rich in Pro, Glu or Asp, Ser and Thr. Z70PEP shares about 70% sequence identity with the human cytoplasmic phosphatase Lyp1. Lyp proteins are important for regulation of T cell antigen and cytokine receptor signalling and for early and late stages of T cell differentiation. Z70PEP has immunosuppressive activity. Compounds that increase expression of Lyp protein can be used as immunosuppressive agents to reduce or prevent T cell activation or proliferation, to control thymocyte differentiation, to treat autoimmune diseases and transplant situations		The present protein sequence is that of the murine phosphatase, Z70PEP that has a single catalytic domain. The non-catalytic portion of the phosphatase contains unique sequences, including five PEST sequences rich in Pro, Glu or Asp, Ser and Thr. Z70PEP shares about 70% sequence identity with the human cytoplasmic phosphatase Lyp1. Lyp proteins are important for regulation of T cell antigen and cytokine receptor signalling and for early and late stages of T cell differentiation. Z70PEP has immunosuppressive activity. Compounds that increase expression of Lyp protein can be used as immunosuppressive agents to reduce or prevent T cell activation or proliferation, to control thymocyte differentiation, to treat autoimmune diseases and transplant situations	
Sequence 802 AA;		Sequence 802 AA;	
Query Match	31.2%; Score 755.5; DB 2; Length 802;	Query Match	31.2%; Score 755.5; DB 2; Length 802;
Best Local Similarity	44.0%; Pred. No. 1.8e-62;	Best Local Similarity	44.0%; Pred. No. 1.8e-62;
Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;		Matches 161; Conservative 55; Mismatches 119; Indels 31; Gaps 7;	
27 AGFSDIQCSAAWKADGVCSTVAGSRDENVRKNRYKVLVDQTRVLSLLCESGSDY 86		27 AGFSDIQCSAAWKADGVCSTVAGSRDENVRKNRYKVLVDQTRVLSLLCESGSDY 86	
25 ASBFLKQSTKYKADKIYPTTVAORPKNIKNRYKILPYDHSLSVLSLTSDESSY 84		25 ASBFLKQSTKYKADKIYPTTVAORPKNIKNRYKILPYDHSLSVLSLTSDESSY 84	

QY	87	INGNIRGVGDSLAYIATQGGPLPHTLLDFWRLVWFGVKVILMACREIENGKCKERYWA	146
DB	85	INASFIKGVYGPYATQGGPLSTLLDFWRMIWEYRILVIWACMEPEMGKKCKERYWA	144
QY	147	QEOE-PLQTGLFCITLKEKWLNEIMLRTIKVTFQKESRSVYQLOYMSWPDGVPSSPD	205
DB	145	EPGETQLOQFPEFSICEAEK-KKSDYKIRTLKAKENNETRIIYQHYKNWPDHVPSSID	203
QY	206	HMLAMVEEARLQSGPEPLCVHCSAGCGRTGVLCTVDYVROLILTOMIPDPFSLFVVL	265
DB	204	PIQLIWNRCYQEDDCVPICHCAGCGRTGVCADVTWMLLKDGIIPKNFSVENLIQ	263
QY	266	KVRKQSPAAVQTEBQYRFYHTVAQMFSTLQNASPHYQNIKENCAPLYDDALFLRTQA	325
DB	264	EMRTQPSLVQTEQVELYSAVLELF-----KRHMDVISDNHLG-----REIQA	308
QY	326	LLAIPEPPGGVLRISVPGS-----PGHAMAD--TYAEQKRGAPAGAGSGTGTGTG	377
DB	309	QCSIPE-----QSLTVEADSCPLDLPKNMVDVKTTHQHSKQGAESTGSSSLGRTS	362
QY	378	ARSAEE 383	
DB	363	TWNAEE 368	
RESULT 7			
AAW89247			
ID	AAW89247	standard; protein; 807 AA.	
XX	AAW89247;		
AC	AAW89247;		
DT	10-MAR-1999	(first entry)	
XX	Human PTP04.		
KW	PTP04; PTP05; SAD; ALP; ALK-7; protein tyrosine phosphatase;		
KW	type I receptor serine/threonine kinase; cancer; leukaemia; lymphoma;		
KW	neurodegenerative disease; neuronal survival; Alzheimer's disease;		
KW	Parkinson's disease; Huntington's disease.		
OS	Homo sapiens.		
XX	WO9849317-A2.		
XX	05-NOV-1998.		
XX	27-APR-1998;	98WO-US008439.	
PR	28-APR-1997;	97US-0044428P.	
PR	20-MAY-1997;	97US-0047222P.	
PR	11-JUN-1997;	97US-0049477P.	
PR	11-JUN-1997;	97US-0049756P.	
PR	18-JUN-1997;	97US-0049914P.	
PR	23-OCT-1997;	97US-0063595P.	
XX	(SUGE-) SUGEN INC.		
XX	Plowman GD, Clary D, Jallal B, Peles E, Onrust S, Markby D;		
PI	Courthridge SA, App H, Hui TH;		
XX	WPI; 1999-009434/01.		
DR	N-PSDB; AAV81742.		
XX	New nucleic acid encoding specific protein tyrosine phosphatases - useful		
PT	for identifying specific modulators for treatment and prevention of		
XX	cancer and neurodegenerative disease.		
XX	Claim 2; Page 151-153; 193pp; English.		
XX	The present invention describes isolated, enriched or purified nucleic		
CC	acids encoding PTP04, SAD, PTP05, PTP10, ALP and ALK-7 proteins. The		
CC	present sequence represents human PTP04. The above proteins, other than		
CC	ALK-7, are protein tyrosine phosphatases (PTPs) and are used to identify		

CC substances that modulate their activity (i.e. agonists and antagonists,
 CC including NBP) in vivo or in vitro. These substances are used to treat or
 CC prevent diseases associated with abnormal signal transduction pathways
 CC that involve the proteins, particularly cancer (e.g. leukaemia and
 CC lymphoma), while modulators of ALK-7 (which is a type I receptor
 CC serine/threonine kinase) are used to promote neuronal survival,
 CC particularly for treating Alzheimer's, Parkinson's or Huntington's
 CC diseases. Nucleic acid fragments of the polynucleotides encoding the
 CC proteins can be used as probes to identify and clone related sequences;
 CC to detect protein-encoded RNA; to generate transgenic animals and in gene
 CC therapy (optionally after mutation). Ab are used to determine the
 CC proteins
 CC
 CC Sequence 807 AA;

Query Match 30.0%; Score 727.5; DB 2; Length 807;
 Best Local Similarity 46.9%; Pred. No. 8.6e-60;
 Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;
 QY 27 AGEFSDIOACSAWKADGVCSTVAGSRPENVRKRYKDVLPYDQTRVILSLQEGHSDY 86
 DB 25 ANEFLLKQSTYKADKTYPTTVAEKPNKIKQRYKDIPLYDSRVLSLITSEDSY 84
 QY 87 INGNFIRGVDGLAYIATQGPLHTLLDFWLVWFGVKVILMACREIENGRKRCERYWA 146
 DB 85 INANFIKGVYGPAYIATQGPLSTLLDFWRMIWEYSVLLIIVMACMEYEMGKKCERYWA 144
 QY 147 QEOE-PLQTGLFCITLIEKWLNEIDIMLTAKVTFQKESRSVYQLYKSWDPGRVPSPD 205
 DB 145 EPGEMOLEFGPPSVSCEAEK-RKSDYIIITLKVFNSETRTIYQFYKNWPDHDPVSSID 203
 QY 206 HMLAMVEEARLQGGPPLCVHCSAGCGRTGVLCTVDYVRLQLLTQMIIPDFSLFDVVL 265
 DB 204 PILELWVRCVQEDDSVPICHCSCGRTGVCICAIDYTWMLLKDGIIPENFSVFLIR 263
 QY 266 KKKORPAAVQTEEQRYFLYHTVQMF---CSTLONASPHYQNIKENCAP 312
 DB 264 EMRTQPSLVQTEQYELVYNAVLELFRQMDVIRDKHSGTSGAQKHCIP 313

RESULT 8

AAG78623
 ID AAG78623 standard; protein; 799 AA.

AC AAG78623;

DT 04-DEC-2001 (first entry)

DE Human tyrosine phosphatase.

KW Human; tyrosine phosphatase; hPTP.

OS Homo sapiens.

PN CN1302899-A.

PD 11-JUL-2001.

PF 29-OCT-1999; 99CN-00119935.

PR 29-OCT-1999; 99CN-00119935.

PA (NANF-) NANFANG RES CENT STATE HUMAN GENE GROUP.

PI Ren S, Wu T, Qian B;

DR WPI; 2001-550591/62.

DR N-PSDB; AAH79342.

PT Human protein tyrosine phosphatase and its coding sequence.

PS Claim 4; Page 12-13 (Disclosure); 29pp; Chinese.

CC The present invention provides the protein and coding sequences of human
 CC tyrosine phosphatase hPTP. The protein is expressed in human normal
 CC suprarenal tissue. The present sequence is the protein of the invention
 CC
 CC Sequence 799 AA;

Query Match 30.0%; Score 726.5; DB 4; Length 799;
 Best Local Similarity 46.9%; Pred. No. 1.1e-59;
 Matches 136; Conservative 56; Mismatches 93; Indels 5; Gaps 3;

QY 27 AGEFSDIOACSAWKADGVCSTVAGSRPENVRKRYKDVLPYDQTRVILSLQEGHSDY 86
 DB 25 ANEFLLKQSTYKADKTYPTTVAEKPNKIKQRYKDIPLYDSRVLSLITSEDSY 84
 QY 87 INGNFIRGVDGLAYIATQGPLHTLLDFWLVWFGVKVILMACREIENGRKRCERYWA 146
 DB 85 INANFIKGVYGPAYIATQGPLSTLLDFWRMIWEYSVLLIIVMACMEYEMGKKCERYWA 144
 QY 147 QEOE-PLQTGLFCITLIEKWLNEIDIMLTAKVTFQKESRSVYQLYKSWDPGRVPSPD 205
 DB 145 EPGEMOLEFGPPSVSCEAEK-RKSDYIIITLKVFNSETRTIYQFYKNWPDHDPVSSID 203
 QY 206 HMLAMVEEARLQGGPPLCVHCSAGCGRTGVLCTVDYVRLQLLTQMIIPDFSLFDVVL 265
 DB 204 PILELWVRCVQEDDSVPICHCSCGRTGVCICAIDYTWMLLKDGIIPENFSVFLIR 263
 QY 266 KKKORPAAVQTEEQRYFLYHTVQMF---CSTLONASPHYQNIKENCAP 312
 DB 264 EMRTQPSLVQTEQYELVYNAVLELFRQMDVIRDKHSGTSGAQKHCIP 313

RESULT 9

ABB57374
 ID ABB57374 standard; protein; 773 AA.

AC ABB57374;

DT 07-MAR-2002 (first entry)

DE Mouse ischaemic condition related protein sequence SEQ ID NO:1064.

KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease.

OS Mus musculus.

PN WO200188188-A2.

PD 22-NOV-2001.

PF 18-MAY-2001; 2001WO-JP004192.

PR 18-MAY-2000; 2000JP-00145977.

PA (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.

PI Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;

DR WPI; 2002-034733/04.

DR N-PSDB; ABI99910.

PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.

PS Claim 2; Page 2685-2689; 2690pp; English.

CC The present invention describes a method for examining ischaemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (I) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (I). The method
 CC is useful for examining the ischaemic condition (e.g. compressive

CC ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
CC expression levels of particular genes (ABI99202 to ABI9912, encoding the
CC protein sequences in AB57020 to AB57374) or by determining the
CC expression profile of a gene group comprising these genes. The expression
CC levels or expression profiles produced by these genes are used as an
CC indicator when screening for ischaemic condition-improving drugs or
CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
CC primers for a mouse ischaemic condition related sequence, which are used
CC in the exemplification of the present invention
XX
SQ Sequence 773 AA;

Query Match 29.3%; Score 710; DB 5; Length 773;
Best Local Similarity 25.4%; Pred. NO. 3.8e-58;
Matches 195; Conservative 88; Mismatches 162; Indels 324; Gaps 20;

QY 9 RSEFLERLEA-----RGGREGAVLAGEFSDIQACSAAKADGVCSTVAGSRPENVRKRYK 63
Db 8 RRFQIRVQAKSPDHNGEDN--FADFVRLRLSTKYRTEKIYPTATGEKEENVKRYK 65

QY 64 DVLPTDQTRVLSLLQESGSHDYNGNFIIRGVDSGLAYIATQGLPHLTLDFLWVBF 123
Db 66 DILPFDHGRVXLTLTQPSQDSYINANFIKGYGPKAYVATQGPFRNTVIDFWMIEYN 125

QY 124 VKVILMACREIENGKRCERYW-AQEQLPQTGFCITLKEKWLNEIDLRLTKVTFQK 182
Db 126 VVMIVNACREEMGRKKERYWPLYGEDPITFAPFKISCENEQ-ARTDYFRTLLLEFQN 184

QY 183 ESRVYQYQYMSWPRGVPSPDHMLANVEEARLQSGPEPLCVHCSAGCGRTGLVCT 242
Db 185 ESRRLYQHYVNWPDHDPVSSFDLSILMKYQEHEDVPICHCAGCGRTGAICAI 244

QY 243 DTVRQLLTQMPDPFSLFDVVLKQKORPAQVTEEQRYRPLYHTVQMP----- 292
Db 245 DYTWNLLKAGKIPPEEFNFIQEMRTQHSVQTKQYELVHRAIAOLFENSYNCKFM 304

QY 293 ----- 292
Db 305 EHRSVMVKLEPLLEWSVPLIARLDLSAKAADSXLPCRCGCGRNTTATRTSPGATHPD 364

QY 293 -----CSTLQNAS-----PHYQN----- 305
Db 365 AITFSFLFNVTTCRTVTGTTQSCCTWPHOSNTQPTSTEAMINQRTNGAKSESAIEHID 424

QY 306 --IKENCA-----PL-----YDALLFL-----RT--PQALLA----- 328
Db 425 KKLERNLSFEIKKVPLOEGPKSFDGNTLLNRGHAIKXSASSVVDRTSKQELSAGALK 484

QY 329 -----IPRP-----PGVLRST-----S 341
Db 485 VDDVSNQSCADCSAAHSHREABESSQSNSHTPPRDCPLDKKHVTWSLHGPNATP 544

QY 342 VFGSPGHAMADTY-----AEEQKR----- 360
Db 545 VPDSPPDGKSPDNHSQTLKTVSTPNSTABEEAHDTEHNSPLKAPLSFTNPLHSDW 604

QY 361 ----GAPAGAGSGTGTGTGA-----RSAAEAPLYSKVTPR-----AQRP 397
Db 605 HSDGSSDGAVENTKTSISTASATVSPASSAESACHRRVLPMSIARQEVAGTFPHSGAEKD 664

QY 398 GAHAEDARTLPCRV----- 413
Db 665 ADVSESPPLPRTPESEFLADMPVRPEWHLPNQWSEQRSEGLTTSNGNEKHDAAGI 724

QY 414 ----ADQSPAGSAGVEDVA-GGAQTGGGFLNLRIGRPGKPRDPPAEWT 456
Db 725 HTEASADSPAPSDKXDKQITKPAEVDIDGFGNRCKGPKGPREPPSEWT 773

RESULT 10
AAY67252
ID AAY67252 standard; protein; 780 AA.
XX

AC AAY67252;
XX 05-APR-2000 (first entry)
DT Human protein tyrosine phosphatase (PTP) PEST amino acid sequence.
DE
XX Protein tyrosine phosphatase; PTP; PEST; paxillin binding; adhesion;
KW cell migration; division; cytostatic; antiinflammatory; angiogenesis;
KW cancer; enzyme substrate identification; human.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Domain 333..340
FT /label=Pro.1
FT /note="Proline rich domain 1"
FT Domain 356..365
FT /label=Pro.2
FT /note="Proline rich domain 2"
FT Domain 519..528
FT /label=Pro.3
FT /note="Proline rich domain 3"
FT Domain 674..680
FT /label=Pro.4
FT /note="Proline rich domain 4"
FT Domain 769..776
FT /label=Pro.5
FT /note="Proline rich domain 5"
XX WO9961467-A2.
XX 02-DEC-1999.
XX 21-MAY-1999; 99WO-CA000461.
XX 21-MAY-1998; 98CA-02238654.
XX 11-DEC-1998; 98US-0111993P.
XX (UYMC-) UNIV MCGILL.
XX Tremblay ML, Cote J, Angers-Lousteau A, Charest A;
XX WPI; 2000-097104/08.
XX Novel therapeutic agents for treating diseases which are related to cell
XX proliferation, migration, inflammation and angiogenesis especially
XX cancer.
XX Claim 4; Fig 24; 91pp; English.
XX
XX This is the amino acid sequence of human protein tyrosine phosphatase
XX (PTP) PEST. PTP-PEST is a soluble PTP that is ubiquitously expressed
XX throughout embryonic development and in murine adult tissues. The N-
XX terminal portion of the enzyme encodes for the catalytic domain, while
XX the C-terminal portion is composed of 5 proline rich domains, and a
XX binding site for the adaptor protein Shc. The pro 2 domain is required
XX for paxillin binding, and the synthesis of mutant PTP-PEST have shown
XX that proline 362 is important for paxillin binding activity. The
XX invention relates to a compound that is capable of interfering with the
XX binding of PTP-PEST to signalling molecules that are involved in cell
XX migration, adhesion or division. The compound can be derived from minimal
XX sequences found in binding sites of PTP-PEST. The invention also relates
XX to a method for finding a genuine substrate for an enzyme in a cell that
XX normally expresses the wild type form of the enzyme. A mutant version of
XX PTP-PEST (see AAY67251 and AAY67253) is used in this method. The
XX compounds have cytostatic and antiinflammatory activity. The compounds
XX are used for making medicaments for treating a disease related with cell
XX proliferation, migration, inflammation and angiogenesis, especially
XX cancer. The novel method is used for identifying a genuine substrate for
XX an enzyme
XX
XX Sequence 780 AA;

PR 16-JAN-1998; 98CA-02220853.
 XX (HSCR-) HSC RES & DEV LP.
 XX Roifman CM;
 XX WPI; 1999-444404/37.
 DR N-PSDB; AAX90696.
 XX New nucleic acid encoding intracellular tyrosine phosphatase and related
 PT proteins, used to modulate signaling through T cells, particularly as
 PT immunosuppressant.
 XX Claim 4b; Page 55; 105pp; English.
 PS
 CC The present protein sequence is that of the cytoplasmic, lymphoid protein
 CC Tyrosine Phosphatase, Lyp2 protein that has a single catalytic domain.
 CC The non-catalytic portion of the phosphatase contains unique sequences,
 CC including a single PEST sequence rich in Pro, Glu or Asp, Ser and Thr. It
 CC is expressed significantly in fetal liver and in resting lymphoid cells.
 CC Lyp2 is an isoform of the Lyp1 gene that arises by alternative splicing
 CC of the mRNA. The intronic sequence of Lyp1 encodes for the C-terminal 7
 CC aminoacids and part of the 3'untranslated region of Lyp2. Lyp2 shares
 CC sequence identity with the murine phosphatase Z703EP. Lyp proteins are
 CC important for regulation of T cell antigen and cytokine receptor
 CC signaling and for early and late stages of T cell differentiation. Lyp2
 CC has immunosuppressive activity. Compounds that increase expression of Lyp
 CC protein can be used as immunosuppressive agents to reduce or prevent T
 CC cell activation or proliferation, to control thymocyte differentiation,
 CC to treat autoimmune diseases and transplant situations
 XX Sequence 692 AA;
 SQ
 Query Match 29.2%; Score 708; DB 2; Length 692;
 Best Local Similarity 46.7%; Pred. NO. 5e-59;
 Matches 136; Conservative 54; Mismatches 95; Indels 6; Gaps 4;
 QY 27 AGFSDIOACSAAWKADGVCSTVAGSRPENTVRKRYKDVLPDQTRVLSLQEGHSDY 86
 DB 25 ANEFLKLRQSTKYKADKTYPTVAENAKNKONKDKILPDYSRVLSLITSDSSY 84
 QY 87 INGNIRGVGSLAYIATQGPLHTLLDFWRLVWVEFGVKVILMACREIENGKRCERYWA 146
 DB 85 INANIKGVYGPKAYIATQGPLSTLLDFWRLVWVEFVLIIVMACMEYEMGKKCERYWA 144
 QY 147 QEQE-PLQTGLFCITLKEKWNEDIMLRTLVKTPQKESRSVYQLQYMSWPDGVPSPD 205
 DB 145 EPGEMQLBFGPPSVSCEAEK-RKSDYIIRTLKVKFNSETRTIYQHYKNWPDHDPSSID 203
 QY 206 HMLAMVERARRLQGGSPPLCVHCSAGCGRTGLCT-VDYVRQLLLTOMIPDPSLFDVW 264
 DB 204 PILELIWVRVCYQEDSDVPICHCAGCGRTGVICAIVDYTWMLLKDGIIENFSVSLI 263
 QY 265 LKVRKQRPAAVQTEEQYRFLYHTVQMFMF---CSTLQNASPHYQNIKENCAP 312
 DB 264 REMRTQRPSELVQSQYELVYNVAVLELPKQMDVIRDKHSGTESQAKHCIP 314
 RESULT 13
 AAM51205
 ID AAM51205 standard; protein; 780 AA.
 XX
 AC AAM51205;
 DT 19-DEC-2001 (first entry)
 XX Human PTP-PEST Gerbank Accession Number XP034191.
 XX PTP; protein tyrosine phosphatase; tyrosine phosphorylated polypeptide;
 KW dephosphorylation; phosphotyrosine; human; PTP-PEST.
 XX Homo sapiens.
 OS
 XX

PN WO200161031-A2.
 XX 23-AUG-2001.
 XX 13-FEB-2001; 2001WO-US005180.
 XX 14-FEB-2000; 2000US-0181769P.
 XX (CEPT-) CEPTYR INC.
 XX Flint AJ, Cool DE;
 XX WPI; 2001-570570/64.
 XX Screening assays to identify agents that alter protein tyrosine
 PT phosphatase (PTP) binding to, and PTP-mediated catalytic
 PT dephosphorylation of phosphotyrosine peptide substrates.
 XX Example 1; Page; 79pp; English.
 XX The invention relates to identifying agents which alter the interaction
 CC between a protein tyrosine phosphatase (PTP) and a tyrosine
 CC phosphorylated polypeptide using fluorescence energy signals. The methods
 CC are useful for performing screening assay to identify agents that alter
 CC PTP binding to and PTP-mediated catalytic dephosphorylation of
 CC phosphotyrosine peptide substrates. The present sequence is not given in
 CC the specification but is that of human PTP-PEST protein sequence taken
 CC from Genbank (Accession Number; XP034191). The present sequence was used
 CC to generate mutants D199A (AAM51201) and C231S (AAM51202) as described in
 CC the specification. Note: An alternative sequence for human PTP-PEST is
 CC given in figure 1 of the specification (AAG78281)
 XX Sequence 780 AA;
 SQ
 Query Match 29.2%; Score 708; DB 4; Length 780;
 Best Local Similarity 40.7%; Pred. NO. 5.9e-58;
 Matches 143; Conservative 66; Mismatches 116; Indels 26; Gaps 7;
 QY 9 RSFLERLEA-----RGREGAVLAGEFSDIQACSAAWKADGVCSTVAGSRPENVRNRYK 63
 DB 8 RKFIQRVQAMKSPDHNGEDN--FARDFMELRLRLSTKYRTEKIYPTATGKEENVKKNRYK 65
 QY 64 DVLPDQTRVLSLQEGHSDYINGNIRGVGSLAYIATQGPLHTLLDFWRLVWVEFG 123
 DB 66 DILPFDHRSVKLTKTPSQDSYINANFIKGVYGPKAYVATQGPLANTVIDFWRMIWEYN 125
 QY 124 VKVILMACREIENGKRCERYW-AQOEPLQTGLFCITLKEKWNEDIMLRTLVKTPQK 182
 DB 126 VTIIVMACREFFEMGRKKERYNPLYGEDPITTFAPFKIS-CEDEQARTDYFIRTLLEFON 184
 QY 183 ESRSVYQLQYMSWPDGVPSPDPHMLAMVEEARLQGGSPPEPLCVHCSAGCGRTGLVCTV 242
 DB 185 ESRRLYQFHYVNPDPHDVDFSSFDSDILMSLRKYQEHEDVPICHCAGCGRTGAICAI 244
 QY 243 DYVRQLLLTOMIPDPSLFDVWLKMKQRPAAVQTEEQYRFLYHTVQMFCSTLQNASPH 302
 DB 245 DYTWMLLKAGKIPEEFNVFNLIQEMRTQKHSVQTEKEQVELVHRAIAQLFEKQLQLEYIH 304
 QY 303 YQNIKENCAPLYDDALFLATPQALLAI-----PRPPGGVLRISIVPG 344
 DB 305 -----GAQKIADGVNEINTNMVSSIEPEKQDSPPKPPR--TRSLVEG 347
 RESULT 14
 AAY28652
 ID AAY28652 standard; protein; 808 AA.
 XX
 AC AAY28652;
 DT 01-OCT-1999 (first entry)
 XX Human Cytoplasmic phosphatase, Lyp1 protein.
 DE
 XX

Lymphoid Protein Tyrosine Phosphatase; Lyp protein; lymphoid cell; intracellular tyrosine phosphatase; PTPase; lymphocyte; thymocyte; T cell; B cell; protein tyrosine kinase; PKs; immunosuppressant; T cell antigen receptor signalling; cytokine receptor signalling; autoimmune disease; transplant.

Homo sapiens.

Key Location/Qualifiers

Domain /label= PTPase domain

note= "Single catalytic protein tyrosine phosphatase domain"

Domain 469..472

note= NXXY motif

note= "Unique sequence recognised by phosphotyrosine binding (PTB) domain"

Binding-site 615..623

/label= SH3 binding site

/note= "Proline rich sequence"

Binding-site 694..701

/label= SH3 binding site

/note= "Proline rich sequence"

Region 702..736

/label= PEST sequence

note= "Sequence rich in Pro, Glu or Asp, Ser and Thr"

Region 741..745

note= "Consensus sequence recognised by p34cdc2 kinase"

Binding-site 768..772

/label= SH3 binding site

/note= "Proline rich sequence"

Binding-site 796..804

/label= SH3 binding site

/note= "Proline rich sequence"

WO9936548-A1.

22-JUL-1999.

18-JAN-1999; 99WO-CA000038.

16-JAN-1998; 98CA-02220853.

(HSCR-) HSC RES & DEV LP.

Roifman CM;

WPI; 1999-444404/37.

N-PSDB; AAX90695.

New nucleic acid encoding intracellular tyrosine phosphatase and related proteins, used to modulate signaling through T cells, particularly as immunosuppressant.

Claim 4a; Page 53; 105pp; English.

The present protein sequence is that of the cytoplasmic, Lymphoid Protein Tyrosine Phosphatase Lyp1, that has a single catalytic domain. The non-catalytic portion of the phosphatase contains unique sequences, including a single PEST sequence rich in Pro, Glu or Asp, Ser and Thr. Lyp1 is expressed in the lymphoid cells, particularly in thymocytes, mature B and T cells and expression is increased upon activation. It is involved in lymphocyte growth and development and is phosphorylated in a cell cycle dependent manner. Lyp1 shares about 70% sequence identity with the murine phosphatase 270Pp. Lyp proteins are important for regulation of T cell antigen and cytokine receptor signalling and for early and late stages of T cell differentiation. Lyp1 has immunosuppressive activity. Compounds that increase expression of Lyp protein can be used as immunosuppressive agents to reduce or prevent T cell activation or proliferation, to control thymocyte differentiation and to treat autoimmune diseases and transplant situations

Sequence 808 AA;

Query Match	29.2%;	Score 708;	DB 2;	Length 808;
Best Local Similarity	46.7%;	Pred. No. 6.2e-58;		
Matches 136;	Conservative 54;	Mismatches 95;	Indels 6;	Gaps 4;
QY	27	AGEFSDIQACSAAWKADGVCSTVAGSRPENVRKRYKQVLFPYDQTRVILSLQEGHSDY	86	
DB	25	ANEFLKLRQSTKYKADTKYPTTVAENAKNKKRYKQILPYDSRVLSLTSDESSY	84	
QY	87	INGNFIRGVDGLAYIATQGPLHTLLDFWRLWVEFGVKVILMACREIENGKRKCRERYWA	146	
DB	85	INANFIKGVYGPXAYIATQGPLSTLLDFWRLWVEYVLIIVMACWEYEMGKKCRERYWA	144	
QY	147	QSOE-PLQTGLFCITLKEKWLNEIMLTLLKVTQKSSRSVYQYMSWDRGVPSSPD	205	
DB	145	EPGEMQLEFGPFSVCEAEK-RKSDYIIITLKVFENSETRTIYQHYQWPDHVPSSID	203	
QY	206	HMLAMVEEARLQGGSPCLVCHCSAGCGRTGVLCT-VDYVRQLLTQMIIPDPSLFDVW	264	
DB	204	PILELIWVRCVQEDDSVPICHCAGCGRTGVI-CAIVDYTWMLLKDGIINENFSVFLI	263	
QY	265	LKVRKQRPAAVQTEBYRYLHYTVAQMF---CSTLQNASPHYQNIKENCAP	312	
DB	264	REMRTPRSLVQTRQYELVYNAVLELFRQMDVIRDKHSGTESQAKHCIP	314	
RESULT 15				
AAV67250				
ID	RAY67250	standard; protein; 775 AA.		
XX	AC	AAV67250;		
XX	DT	05-APR-2000 (first entry)		
XX	DE	Mouse protein tyrosine phosphatase (PTP) PEST amino acid sequence.		
XX	KW	Protein tyrosine phosphatase; PTP; PEST; paxillin binding; adhesion;		
XX	KW	cell migration; division; cytostatic; antiinflammatory; angiogenesis;		
XX	KW	cancer; enzyme substrate identification; mouse.		
XX	OS	Mus sp.		
XX	Key	Location/Qualifiers		
FT	Domain	332..339		
FT		/label= Pro 1		
FT		/note= "Proline rich domain 1"		
FT	Domain	355..364		
FT		/label= Pro 2		
FT		/note= "Proline rich domain 2"		
FT	Domain	519..528		
FT		/label= Pro 3		
FT		/note= "Proline rich domain 3"		
FT	Domain	675..681		
FT		/label= Pro 4		
FT		/note= "Proline rich domain 4"		
FT	Domain	764..771		
FT		/label= Pro 5		
FT		/note= "Proline rich domain 5"		
XX	WO9961467-A2.			
XX	02-DEC-1999.			
XX	21-MAY-1999;	99WO-CA0000461.		
XX	21-MAY-1999;	98CA-02238654.		
XX	11-DEC-1998;	98US-0111993P.		
XX	(UYMC-) UNIV MCGILL.			
XX	Tremblay ML, Cote J, Angers-Lousteau A, Charest A;			
XX	WPI; 2000-097104/08.			

XX Novel therapeutic agents for treating diseases which are related to cell
PT proliferation, migration, inflammation and angiogenesis especially
PT cancer.
XX
PS Claim 4; Fig 24; 91pp; English.
XX
CC This is the amino acid sequence of mouse protein tyrosine phosphatase
CC (PTP). PTP-PEST is a soluble PTP that is ubiquitously expressed
CC throughout embryonic development and in murine adult tissues. The N-
CC terminal portion of the enzyme encodes for the catalytic domain, while
CC the C-terminal portion is composed of 5 proline rich domains, and a
CC binding site for the adaptor protein Shc. The pro 2 domain is required
CC for paxillin binding, and the synthesis of mutant PTP-PEST have shown
CC that proline 362 is important for paxillin binding activity. The
CC invention relates to a compound that is capable of interfering with the
CC binding of PTP-PEST to signalling molecules that are involved in cell
CC migration, adhesion or division. The compound can be derived from minimal
CC sequences found in binding sites of PTP-PEST. The invention also relates
CC to a method for finding a genuine substrate for an enzyme in a cell that
CC normally expresses the wild type form of the enzyme. A mutant version of
CC PTP-PEST (see AY67251 and AY67253) is used in this method. The
CC compounds have cytostatic and antiinflammatory activity. The compounds
CC are used for making medicaments for treating a disease related with cell
CC proliferation, migration, inflammation and angiogenesis, especially
CC cancer. The novel method is used for identifying a genuine substrate for
CC an enzyme
XX
SQ Sequence 775 AA;
Query Match 29.1%; Score 705; DB 3; Length 775;
Best Local Similarity 25.0%; Pred. No. 1.1e-57;
Matches 194; Conservative 84; Mismatches 162; Indels 336; Gaps 17;
QY 9 RSFLERLEA-----RGGREGAVLAGESDIOACSAANKADGVCSTVAGSPENVRKNRYK 63
DB 8 RRFQVQAMKSPDHNGEDN--FARDFWRLRLSTKTKTEKIYPTATGEENVKKNRYK 65
QY 64 DVLPTDQTRVILSLLOEEHSGSDYINGNFRIGVDGSLAYIATQGPLPHTLLDFWRLVWFG 123
DB 66 DILFPDHSRVKLTLPKTSQDSQSDYINANFIKGVYGPAAVATQGPFRNTVIDFWRMIWEYN 125
QY 124 KVVILMACREIENGKRCERYW--KQEQEPLQTGLFCITLKEKWLNEIDMLRTLKVTFOK 182
DB 126 VVIIVMACREFEMGKKCERYWPLYGEDPITFAPFKISCENEQ--ARTDYFIRTLLEFON 184
QY 183 ERSRYVQLQYMSWDRGVPSPDHMLAMVEARLQGSPPCLVCHSGAGCGRTGVLCTV 242
DB 185 ESRRLYQFHYVNVDPHDVPSSFDLSILDMISLWKYQEHEDVPICIHCSAGCGRTGAICAI 244
QY 243 DYVRQLLLTQMPDFSLFDVVLKQRKQRPAAVQTESQYRFLYHTVAQMFCSTLQ----- 297
DB 245 DYTWNLLKAGKIPBEFNFVNLQEMRTQRHSAVQTKQYELVHRAIAQLFEKQLQLYEIH 304
QY 298 ----- 297
DB 305 GAQKIADGNEITGTMTVSSIDSEKQDSPPPKPPTRSCLVGDAKEILQPPPEHPVPPI 364
QY 298 -----NASP----- 301
DB 365 LTPSPSAPFTVTTWQSDRYHPKPVHLHMASPEQHAPDLNRSYDKSQDWGKSESAIEH 424
QY 302 -----HYQNIKENCAPLYDDALFLRT--POA 325
DB 425 IDKKLERNLSPFIKKVPLQEGPKGFDGNTLLNRGHAIKIKSASSSVVD-----RTSKPQE 479
QY 326 LIA-----IPRP-----PGGVLRSI- 340
DB 480 LSAGALKYDDVYQNSCADCSAAHSHRAESSEESQSNSHTPRPDCLPLDKKGHTWSLH 539
QY 341 -----SVPGSPGHAMADTY-----ABEQKR----- 360
DB 540 GPNATPVDPDGPDKGSPNHSQTLKTVSTPNSTAEAEHADLTEHNSSPILLKAPLSFTN 599

QY 361 -----CAPAGASGTGTGTGTA-----RSAEAPLYSKVTPR----- 393
DB 600 PLHSDDMHSDGSGDGAIVTRNKTSISTASATVSPASSAESACHRRVLPMSIARQEVAGTP 659
QY 394 ---AQRPGAHABDARGTLPGRVF----- 413
DB 660 HSGAEKDADVSESPPLPERTFESFVLADMPVRPEWHELPNQEWSEQSESEGLTTSUNE 719
QY 414 -----ADOSPAGSGAYEDVA--GGAQTGGGLGNLAIGRPKGRDPAENT 456
DB 720 KHDAGGIHTASADSPAPFADKKDQITKSPAENVTDIGFNGRCGKPKGPREPPSEWT 775

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